

Please delete the paragraph on page 8, lines 5-7, and replace it with the following paragraph:

FIG. 1 is a schematic of various methods that may be employed to amplify VH genes without using primers specific for VH sequences. The T<sub>15</sub> oligonucleotide is shown in SEQ ID NO: 622.

Please delete the paragraph on page 8, lines 28-29, and replace it with the following paragraph:

FIG. 10 is a schematic of the design for CDR1 and CDR2 synthetic diversity. The YADSVKG peptide is shown in SEQ ID NO: 604.

Please delete the paragraph on page 9, lines 10-12, and replace it with the following paragraph:

FIG. 18 is a schematic of a process for incorporating fixed FR1 residues in an antibody lambda sequence. The PCRpr oligonucleotide is shown in SEQ ID NO: 605 while the Bridge oligonucleotide and encoded peptide are shown in SEQ ID NOS 606-607, respectively.

Please delete the paragraph on page 9, lines 13-15, and replace it with the following paragraph:

FIG. 19 is a schematic of a process for incorporating fixed FR1 residues in an antibody kappa sequence (see SEQ ID NOS 608-611, respectively, in order of appearance).

Please delete the paragraph on page 9, lines 16-18, and replace it with the following paragraph:

FIG. 20 is a schematic of a process for incorporating fixed FR1 residues in an antibody heavy chain sequence. The PCRpr oligonucleotide is shown in SEQ ID NO: 612. The Bridge

oligonucleotides are shown in SEQ ID NOS 613 & 615, respectively, in order of appearance, while the encoded peptides are shown in SEQ ID NOS 614 & 616, respectively, in order of appearance.

Please delete the paragraph on page 56, line 9, to page 57, line 3, and replace it with the following paragraph:

After bla, is the Fab cassette (illustrated in FIG. 17) comprising:

- a) PlacZ promoter,
- b) A first Ribosome Binding Site (RBS1),
- c) The signal sequence form M13 iii,
- d) An *ApaLI* RERS,
- e) A light chain (a kappa L20::JK1 shortened by one codon at the V-J boundary in this case),
- f) An *AscI* RERS,
- g) A second Ribosome Binding Site (RBS2),
- h) A signal sequence, preferably PelB, which contains,
- i) An *SfiI* RERS,
- j) A synthetic 3-23 V region with diversity in CDR1 and CDR2,
- k) A captured CDR3,
- l) A partially synthetic J region (FR4 after *BstEII*),
- m) CH1,
- n) A *NotI* RERS,
- o) A His6 tag (SEQ ID NO: 12),
- p) A cMyc tag,
- q) An amber codon,
- r) An anchor DNA that encodes the same amino-acid sequence as codons 273 to 424 of M13 iii (as shown in Table 37).
- s) Two stop codons,
- t) An *AvrII* RERS, and
- u) A trp terminator.

Please delete the paragraph on page 58, lines 6-16, and replace it with the following paragraph:

Table 38 shows a gene fragment comprising the *NotI* site, His6 tag (SEQ ID NO: 12), cMyc tag, an amber codon, a recombinant enterokinase cleavage site, and the whole of mature M13 III protein. The DNA used to encode this sequence is intentionally very different from the DNA of wild-type gene iii as shown by the lines denoted "W.T." containing the w.t. bases where these differ from this gene. III is divided into domains denoted "domain 1", "linker 1", "domain 2", "linker 2", "domain 3", "transmembrane segment", and "intracellular anchor".

Please delete the paragraph on page 59, lines 5-23, and replace it with the following paragraph:

The constructs would most readily be made by methods similar to those of Wang and Wilkinson (Biotechniques 2001: 31(4)722-724) in which PCR is used to copy the vector except the part to be deleted and matching restriction sites are introduced or retained at either end of the part to be kept. Table 39 shows the oligonucleotides to be used in deleting parts of the III anchor segment. The DNA shown in Table 38 has an *NheI* site before the DINDDRMA (residues 29-36 of SEQ ID NO: 594) recombinant enterokinase cleavage site (rEKCS). If *NheI* is used in the deletion process with this DNA, the rEKCS site would be lost. This site could be quite useful in cleaving Fabs from the phage and might facilitate capture of very high-affinity antibodies. One could mutagenize this sequence so that the *NheI* site would follow the rEKCS site, an Ala Ser amino-acid sequence is already present. Alternatively, one could use *SphI* for the deletions. This would involve a slight change in amino acid sequence but would be of no consequence.

Please delete Table 1 and replace it with the following table:

Table 1: Human GLG FR3 sequences

! VH1

! 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80  
agg gtc acc atg acc agg gac acg tcc atc agc aca gcc tac atg

! 81 82 82a 82b 82c 83 84 85 86 87 88 89 90 91 92  
gag ctg agc agg ctg aga tct gac gac acg gcc gtg tat tac tgt

! 93 94 95  
gcg aga ga ! 1-02# 1 (SEQ ID NO: 34)  
aga gtc acc att acc agg gac aca tcc gcg agc aca gcc tac atg  
gag ctg agc agc ctg aga tct gaa gac acg gct gtg tat tac tgt  
gcg aga ga ! 1-03# 2 (SEQ ID NO: 35)  
aga gtc acc atg acc agg aac acc tcc ata agc aca gcc tac atg  
gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt  
gcg aga gg ! 1-08# 3 (SEQ ID NO: 36)  
aga gtc acc atg acc aca gac aca tcc acg agc aca gcc tac atg  
gag ctg agg agc ctg aga tct gac gac acg gcc gtg tat tac tgt  
gcg aga ga ! 1-18# 4 (SEQ ID NO: 37)  
aga gtc acc atg acc gag gac aca tct aca gac aca gcc tac atg  
gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt  
gca aca ga ! 1-24# 5 (SEQ ID NO: 38)  
aga gtc acc att acc agg gac agg tct atg agc aca gcc tac atg  
gag ctg agc agc ctg aga tct gag gac aca gcc atg tat tac tgt  
gca aga ta ! 1-45# 6 (SEQ ID NO: 39)  
aga gtc acc atg acc agg gac acg tcc acg agc aca gtc tac atg  
gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt  
gcg aga ga ! 1-46# 7 (SEQ ID NO: 40)  
aga gtc acc att acc agg gac atg tcc aca agc aca gcc tac atg  
gag ctg agc agc ctg aga tcc gag gac acg gcc gtg tat tac tgt  
gcg gca ga ! 1-58# 8 (SEQ ID NO: 41)  
aga gtc acg att acc gcg gac gaa tcc acg agc aca gcc tac atg  
gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt  
gcg aga ga ! 1-69# 9 (SEQ ID NO: 42)  
aga gtc acg att acc gcg gac aaa tcc acg agc aca gcc tac atg  
gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt  
gcg aga ga ! 1-e# 10 (SEQ ID NO: 43)  
aga gtc acc ata acc gcg gac acg tct aca gac aca gcc tac atg  
gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt  
gca aca ga ! 1-f# 11 (SEQ ID NO: 44)

! VH2  
agg ctc acc atc acc aag gac acc tcc aaa aac cag gtg gtc ctt  
aca atg acc aac atg gac cct gtg gac aca gcc aca tat tac tgt  
gca cac aga c! 2-05# 12 (SEQ ID NO: 45)  
agg ctc acc atc tcc aag gac acc tcc aaa agc cag gtg gtc ctt



acc atg acc aac atg gac cct gtg gac aca gcc aca tat tac tgt  
gca cgg ata c! 2-26# 13 (SEQ ID NO: 46)  
agg ctc acc atc tcc aag gac acc tcc aaa aac cag gtg gtc ctt  
aca atg acc aac atg gac cct gtg gac aca gcc acg tat tac tgt  
gca cgg ata c! 2-70# 14 (SEQ ID NO: 47)

! VH3  
cga ttc acc atc tcc aga gac aac gcc aag aac tca ctg tat ctg  
caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt  
gcg aga ga ! 3-07# 15 (SEQ ID NO: 48)  
cga ttc acc atc tcc aga gac aac gcc aag aac tcc ctg tat ctg  
caa atg aac agt ctg aga gct gag gac acg gcc ttg tat tac tgt  
gca aaa gat a! 3-09#16 (SEQ ID NO: 49)  
cga ttc acc atc tcc agg gac aac gcc aag aac tca ctg tat ctg  
caa atg aac agc ctg aga gcc gag gac acg gcc gtg tat tac tgt  
gcg aga ga ! 3-11# 17 (SEQ ID NO: 50)  
cga ttc acc atc tcc aga gaa aat gcc aag aac tcc ttg tat ctt  
caa atg aac agc ctg aga gcc ggg gac acg gct gtg tat tac tgt  
gca aga ga ! 3-13# 18 (SEQ ID NO: 51)  
aga ttc acc atc tca aga gat gat tca aaa aac acg ctg tat ctg  
caa atg aac agc ctg aaa acc gag gac aca gcc gtg tat tac tgt  
acc aca ga ! 3-15# 19 (SEQ ID NO: 52)  
cga ttc acc atc tcc aga gac aac gcc aag aac tcc ctg tat ctg  
caa atg aac agt ctg aga gcc gag gac acg gcc ttg tat cac tgt  
gcg aga ga ! 3-20# 20 (SEQ ID NO: 53)  
cga ttc acc atc tcc aga gac aac gcc aag aac tca ctg tat ctg  
caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt  
gcg aga ga ! 3-21# 21 (SEQ ID NO: 54)  
cgg ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctg  
caa atg aac agc ctg aga gcc gag gac acg gcc gta tat tac tgt  
gcg aaa ga ! 3-23# 22 (SEQ ID NO: 55)  
cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctg  
caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac tgt  
gcg aaa ga ! 3-30# 23 (SEQ ID NO: 56)  
cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctg  
caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac tgt  
gcg aga ga ! 3303# 24 (SEQ ID NO: 57)  
cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctg  
caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac tgt  
gcg aaa ga ! 3305# 25 (SEQ ID NO: 58)  
cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctg  
caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt

gcg aga ga ! 3-33# 26 (SEQ ID NO: 59)  
cga ttc acc atc tcc aga gac aac agc aaa aac tcc ctg tat ctg  
caa atg aac agt ctg aga act gag gac acc gcc ttg tat tac tgt  
gca aaa gat a! 3-43#27 (SEQ ID NO: 60)  
cga ttc acc atc tcc aga gac aat gcc aag aac tca ctg tat ctg  
caa atg aac agc ctg aga gac gag gac acg gct gtg tat tac tgt  
gcg aga ga ! 3-48# 28 (SEQ ID NO: 61)  
aga ttc acc atc tca aga gat ggt tcc aaa agc atc gcc tat ctg  
caa atg aac agc ctg aaa acc gag gac aca gcc gtg tat tac tgt  
act aga ga ! 3-49# 29 (SEQ ID NO: 62)  
cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctt  
caa atg aac agc ctg aga gcc gag gac acg gcc gtg tat tac tgt  
gcg aga ga ! 3-53# 30 (SEQ ID NO: 63)  
aga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctt  
caa atg ggc agc ctg aga gct gag gac atg gct gtg tat tac tgt  
gcg aga ga ! 3-64# 31 (SEQ ID NO: 64)  
aga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctt  
caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac tgt  
gcg aga ga ! 3-66# 32 (SEQ ID NO: 65)  
aga ttc acc atc tca aga gat gat tca aag aac tca ctg tat ctg  
caa atg aac agc ctg aaa acc gag gac acg gcc gtg tat tac tgt  
gct aga ga ! 3-72# 33 (SEQ ID NO: 66)  
agg ttc acc atc tcc aga gat gat tca aag aac acg gcg tat ctg  
caa atg aac agc ctg aaa acc gag gac acg gcc gtg tat tac tgt  
act aga ca ! 3-73# 34 (SEQ ID NO: 67)  
cga ttc acc atc tcc aga gac aac gcc aag aac acg ctg tat ctg  
caa atg aac agt ctg aga gcc gag gac acg gct gtg tat tac tgt  
gca aga ga ! 3-74# 35 (SEQ ID NO: 68)  
aga ttc acc atc tcc aga gac aat tcc aag aac acg ctg cat ctt  
caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac tgt  
aag aaa ga ! 3-d# 36 (SEQ ID NO: 69)

! VH4

cga gtc acc ata tca gta gac aag tcc aag aac cag ttc tcc ctg  
aag ctg agc tct gtg acc gcc gcg gac acg gcc gtg tat tac tgt  
gcg aga ga ! 4-04# 37 (SEQ ID NO: 70)  
cga gtc acc atg tca gta gac acg tcc aag aac cag ttc tcc ctg  
aag ctg agc tct gtg acc gcc gtg gac acg gcc gtg tat tac tgt  
gcg aga aa ! 4-28# 38 (SEQ ID NO: 71)  
cga gtt acc ata tca gta gac acg tct aag aac cag ttc tcc ctg  
aag ctg agc tct gtg act gcc gcg gac acg gcc gtg tat tac tgt  
gcg aga ga ! 4301# 39 (SEQ ID NO: 72)

cga gtc acc ata tca gta gac agg tcc aag aac cag ttc tcc ctg  
aag ctg agc tct gtg acc gcc gcg gac acg gcc gtg tat tac tgt  
gcc aga ga ! 4302# 40 (SEQ ID NO: 73)

cga gtt acc ata tca gta gac acg tcc aag aac cag ttc tcc ctg  
aag ctg agc tct gtg act gcc gca gac acg gcc gtg tat tac tgt  
gcc aga ga ! 4304# 41 (SEQ ID NO: 74)

cga gtt acc ata tca gta gac acg tct aag aac cag ttc tcc ctg  
aag ctg agc tct gtg act gcc gcg gac acg gcc gtg tat tac tgt  
gcg aga ga ! 4-31# 42 (SEQ ID NO: 75)

cga gtc acc ata tca gta gac acg tcc aag aac cag ttc tcc ctg  
aag ctg agc tct gtg acc gcc gcg gac acg gct gtg tat tac tgt  
gcg aga ga ! 4-34# 43 (SEQ ID NO: 76)

cga gtc acc ata tcc gta gac acg tcc aag aac cag ttc tcc ctg  
aag ctg agc tct gtg acc gcc gca gac acg gct gtg tat tac tgt  
gcg aga ca ! 4-39# 44 (SEQ ID NO: 77)

cga gtc acc ata tca gta gac acg tcc aag aac cag ttc tcc ctg  
aag ctg agc tct gtg acc gct gcg gac acg gcc gtg tat tac tgt  
gcg aga ga ! 4-59# 45 (SEQ ID NO: 78)

cga gtc acc ata tca gta gac acg tcc aag aac cag ttc tcc ctg  
aag ctg agc tct gtg acc gct gcg gac acg gcc gtg tat tac tgt  
gcg aga ga ! 4-61# 46 (SEQ ID NO: 79)

cga gtc acc ata tca gta gac acg tcc aag aac cag ttc tcc ctg  
aag ctg agc tct gtg acc gcc gca gac acg gcc gtg tat tac tgt  
gcg aga ga ! 4-b# 47 (SEQ ID NO: 80)

! VH5

cag gtc acc atc tca gcc gac aag tcc atc agc acc gcc tac ctg  
cag tgg agc agc ctg aag gcc tcg gac acc gcc atg tat tac tgt  
gcg aga ca ! 5-51# 48 (SEQ ID NO: 81)

cac gtc acc atc tca gct gac aag tcc atc agc act gcc tac ctg  
cag tgg agc agc ctg aag gcc tcg gac acc gcc atg tat tac tgt  
gcg aga ! 5-a# 49 (SEQ ID NO: 82)

! VH6

cga ata acc atc aac cca gac aca tcc aag aac cag ttc tcc ctg  
cag ctg aac tct gtg act ccc gag gac acg gct gtg tat tac tgt  
gca aga ga ! 6-1# 50 (SEQ ID NO: 83)

! VH7

cgg ttt gtc ttc tcc ttg gac acc tct gtc agc acg gca tat ctg  
cag atc tgc agc cta aag gct gag gac act gcc gtg tat tac tgt  
gcg aga ga ! 74.1# 51 (SEQ ID NO: 84)

Please delete Table 2 and replace it with the following table:

Table 2: Enzymes that either cut 15 or more human GLGs or have 5+-base recognition in FR3

Typical entry:

REname Recognition		#sites
GLGid#:base#	GLGid#:base#	GLGid#:base#.....

BstEII	Ggtnacc	2
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1: 3 48: 3

There are 2 hits at base# 3

MaeIII	gtnac	36
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1: 4	2: 4	3: 4	4: 4	5: 4	6: 4
7: 4	8: 4	9: 4	10: 4	11: 4	37: 4
37: 58	38: 4	38: 58	39: 4	39: 58	40: 4
40: 58	41: 4	41: 58	42: 4	42: 58	43: 4
43: 58	44: 4	44: 58	45: 4	45: 58	46: 4
46: 58	47: 4	47: 58	48: 4	49: 4	50: 58

There are 24 hits at base# 4

Tsp45I	gtsac	33
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1: 4	2: 4	3: 4	4: 4	5: 4	6: 4
7: 4	8: 4	9: 4	10: 4	11: 4	37: 4
37: 58	38: 4	38: 58	39: 58	40: 4	40: 58
41: 58	42: 58	43: 4	43: 58	44: 4	44: 58
45: 4	45: 58	46: 4	46: 58	47: 4	47: 58
48: 4	49: 4	50: 58			

There are 21 hits at base# 4

HphI	tcacc	45
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1: 5	2: 5	3: 5	4: 5	5: 5	6: 5
7: 5	8: 5	11: 5	12: 5	12: 11	13: 5
14: 5	15: 5	16: 5	17: 5	18: 5	19: 5
20: 5	21: 5	22: 5	23: 5	24: 5	25: 5
26: 5	27: 5	28: 5	29: 5	30: 5	31: 5
32: 5	33: 5	34: 5	35: 5	36: 5	37: 5
38: 5	40: 5	43: 5	44: 5	45: 5	46: 5

47: 5 48: 5 49: 5

There are 44 hits at base# 5

NlaIII CATG

26

1: 9 1: 42 2: 42 3: 9 3: 42 4: 9  
4: 42 5: 9 5: 42 6: 42 6: 78 7: 9  
7: 42 8: 21 8: 42 9: 42 10: 42 11: 42  
12: 57 13: 48 13: 57 14: 57 31: 72 38: 9  
48: 78 49: 78

There are 11 hits at base# 42

There are 1 hits at base# 48 Could cause raggedness.

BsaJI Ccnngg

37

1: 14 2: 14 5: 14 6: 14 7: 14 8: 14  
8: 65 9: 14 10: 14 11: 14 12: 14 13: 14  
14: 14 15: 65 17: 14 17: 65 18: 65 19: 65  
20: 65 21: 65 22: 65 26: 65 29: 65 30: 65  
33: 65 34: 65 35: 65 37: 65 38: 65 39: 65  
40: 65 42: 65 43: 65 48: 65 49: 65 50: 65  
51: 14

There are 23 hits at base# 65

There are 14 hits at base# 14

AluI AGct

42

1: 47 2: 47 3: 47 4: 47 5: 47 6: 47  
7: 47 8: 47 9: 47 10: 47 11: 47 16: 63  
23: 63 24: 63 25: 63 31: 63 32: 63 36: 63  
37: 47 37: 52 38: 47 38: 52 39: 47 39: 52  
40: 47 40: 52 41: 47 41: 52 42: 47 42: 52  
43: 47 43: 52 44: 47 44: 52 45: 47 45: 52  
46: 47 46: 52 47: 47 47: 52 49: 15 50: 47

There are 23 hits at base# 47

There are 11 hits at base# 52 Only 5 bases from 47

BlpI GCTnagc

21

1: 48 2: 48 3: 48 5: 48 6: 48 7: 48  
8: 48 9: 48 10: 48 11: 48 37: 48 38: 48  
39: 48 40: 48 41: 48 42: 48 43: 48 44: 48  
45: 48 46: 48 47: 48

There are 21 hits at base# 48

MwoI GCNNNNNnngc(SEQ ID NO:85) 19

1: 48    2: 28    19: 36    22: 36    23: 36    24: 36  
25: 36    26: 36    35: 36    37: 67    39: 67    40: 67  
41: 67    42: 67    43: 67    44: 67    45: 67    46: 67  
47: 67

There are 10 hits at base# 67

There are 7 hits at base# 36

DdeI Ctnag 71

1: 49    1: 58    2: 49    2: 58    3: 49    3: 58  
3: 65    4: 49    4: 58    5: 49    5: 58    5: 65  
6: 49    6: 58    6: 65    7: 49    7: 58    7: 65  
8: 49    8: 58    9: 49    9: 58    9: 65    10: 49  
10: 58    10: 65    11: 49    11: 58    11: 65    15: 58  
16: 58    16: 65    17: 58    18: 58    20: 58    21: 58  
22: 58    23: 58    23: 65    24: 58    24: 65    25: 58  
25: 65    26: 58    27: 58    27: 65    28: 58    30: 58  
31: 58    31: 65    32: 58    32: 65    35: 58    36: 58  
36: 65    37: 49    38: 49    39: 26    39: 49    40: 49  
41: 49    42: 26    42: 49    43: 49    44: 49    45: 49  
46: 49    47: 49    48: 12    49: 12    51: 65

There are 29 hits at base# 58

There are 22 hits at base# 49 Only nine base from 58

There are 16 hits at base# 65 Only seven bases from 58

BglIII Agatct 11

1: 61    2: 61    3: 61    4: 61    5: 61    6: 61  
7: 61    9: 61    10: 61    11: 61    51: 47

There are 10 hits at base# 61

BstYI Rgatcy 12

1: 61    2: 61    3: 61    4: 61    5: 61    6: 61  
7: 61    8: 61    9: 61    10: 61    11: 61    51: 47

There are 11 hits at base# 61

Hpy188I TCNGa 17

1: 64	2: 64	3: 64	4: 64	5: 64	6: 64
7: 64	8: 64	9: 64	10: 64	11: 64	16: 57
20: 57	27: 57	35: 57	48: 67	49: 67	

There are 11 hits at base# 64

There are 4 hits at base# 57

There are 2 hits at base# 67 Could be ragged.

MslI CAYNNnnRTG (SEQ ID NO:86) 44

1: 72	2: 72	3: 72	4: 72	5: 72	6: 72
7: 72	8: 72	9: 72	10: 72	11: 72	15: 72
17: 72	18: 72	19: 72	21: 72	23: 72	24: 72
25: 72	26: 72	28: 72	29: 72	30: 72	31: 72
32: 72	33: 72	34: 72	35: 72	36: 72	37: 72
38: 72	39: 72	40: 72	41: 72	42: 72	43: 72
44: 72	45: 72	46: 72	47: 72	48: 72	49: 72
50: 72	51: 72				

There are 44 hits at base# 72

BsiEI CGRYcg 23

1: 74	3: 74	4: 74	5: 74	7: 74	8: 74
9: 74	10: 74	11: 74	17: 74	22: 74	30: 74
33: 74	34: 74	37: 74	38: 74	39: 74	40: 74
41: 74	42: 74	45: 74	46: 74	47: 74	

There are 23 hits at base# 74

EaeI Yggccr 23

1: 74	3: 74	4: 74	5: 74	7: 74	8: 74
9: 74	10: 74	11: 74	17: 74	22: 74	30: 74
33: 74	34: 74	37: 74	38: 74	39: 74	40: 74
41: 74	42: 74	45: 74	46: 74	47: 74	

There are 23 hits at base# 74

EagI Cggccg 23

1: 74	3: 74	4: 74	5: 74	7: 74	8: 74
9: 74	10: 74	11: 74	17: 74	22: 74	30: 74
33: 74	34: 74	37: 74	38: 74	39: 74	40: 74
41: 74	42: 74	45: 74	46: 74	47: 74	

There are 23 hits at base# 74

HaeIII GGcc

27

1: 75	3: 75	4: 75	5: 75	7: 75	8: 75
9: 75	10: 75	11: 75	16: 75	17: 75	20: 75
22: 75	30: 75	33: 75	34: 75	37: 75	38: 75
39: 75	40: 75	41: 75	42: 75	45: 75	46: 75
47: 75	48: 63	49: 63			

There are 25 hits at base# 75

Bst4CI ACNgt 65°C

63 Sites There is a third isoschismer

1: 86	2: 86	3: 86	4: 86	5: 86	6: 86
7: 34	7: 86	8: 86	9: 86	10: 86	11: 86
12: 86	13: 86	14: 86	15: 36	15: 86	16: 53
16: 86	17: 36	17: 86	18: 86	19: 86	20: 53
20: 86	21: 36	21: 86	22: 0	22: 86	23: 86
24: 86	25: 86	26: 86	27: 53	27: 86	28: 36
28: 86	29: 86	30: 86	31: 86	32: 86	33: 36
33: 86	34: 86	35: 53	35: 86	36: 86	37: 86
38: 86	39: 86	40: 86	41: 86	42: 86	43: 86
44: 86	45: 86	46: 86	47: 86	48: 86	49: 86
50: 86	51: 0	51: 86			

There are 51 hits at base# 86 All the other sites are well away

HpyCH4III ACNgt

63

1: 86	2: 86	3: 86	4: 86	5: 86	6: 86
7: 34	7: 86	8: 86	9: 86	10: 86	11: 86
12: 86	13: 86	14: 86	15: 36	15: 86	16: 53
16: 86	17: 36	17: 86	18: 86	19: 86	20: 53
20: 86	21: 36	21: 86	22: 0	22: 86	23: 86
24: 86	25: 86	26: 86	27: 53	27: 86	28: 36
28: 86	29: 86	30: 86	31: 86	32: 86	33: 36
33: 86	34: 86	35: 53	35: 86	36: 86	37: 86
38: 86	39: 86	40: 86	41: 86	42: 86	43: 86
44: 86	45: 86	46: 86	47: 86	48: 86	49: 86
50: 86	51: 0	51: 86			

There are 51 hits at base# 86



HinfI Gantc 43

2: 2	3: 2	4: 2	5: 2	6: 2	7: 2
8: 2	9: 2	9: 22	10: 2	11: 2	15: 2
16: 2	17: 2	18: 2	19: 2	19: 22	20: 2
21: 2	23: 2	24: 2	25: 2	26: 2	27: 2
28: 2	29: 2	30: 2	31: 2	32: 2	33: 2
33: 22	34: 22	35: 2	36: 2	37: 2	38: 2
40: 2	43: 2	44: 2	45: 2	46: 2	47: 2
50: 60					

There are 38 hits at base# 2

MlyI GAGTCNNNNNNn (SEQ ID NO:87) 18

2: 2	3: 2	4: 2	5: 2	6: 2	7: 2
8: 2	9: 2	10: 2	11: 2	37: 2	38: 2
40: 2	43: 2	44: 2	45: 2	46: 2	47: 2

There are 18 hits at base# 2

PleI gagtc 18

2: 2	3: 2	4: 2	5: 2	6: 2	7: 2
8: 2	9: 2	10: 2	11: 2	37: 2	38: 2
40: 2	43: 2	44: 2	45: 2	46: 2	47: 2

There are 18 hits at base# 2

AciI Ccgc 24

2: 26	9: 14	10: 14	11: 14	27: 74	<u>37: 62</u>
<u>37: 65</u>	38: 62	39: 65	<u>40: 62</u>	<u>40: 65</u>	41: 65
42: 65	<u>43: 62</u>	<u>43: 65</u>	<u>44: 62</u>	<u>44: 65</u>	45: 62
46: 62	<u>47: 62</u>	<u>47: 65</u>	48: 35	48: 74	49: 74

There are 8 hits at base# 62

There are 8 hits at base# 65

There are 3 hits at base# 14

There are 3 hits at base# 74

There are 1 hits at base# 26

There are 1 hits at base# 35

--- Gcgg 11

8: 91	9: 16	10: 16	11: 16	37: 67	39: 67
40: 67	42: 67	43: 67	45: 67	46: 67	

There are 7 hits at base# 67

There are 3 hits at base# 16

There are 1 hits at base# 91

BsiHKAI GWGCWc 20

2: 30	4: 30	6: 30	7: 30	9: 30	10: 30
12: 89	13: 89	14: 89	37: 51	38: 51	39: 51
40: 51	41: 51	42: 51	43: 51	44: 51	45: 51
46: 51	47: 51				

There are 11 hits at base# 51

Bsp1286I GDGCHc 20

2: 30	4: 30	6: 30	7: 30	9: 30	10: 30
12: 89	13: 89	14: 89	37: 51	38: 51	39: 51
40: 51	41: 51	42: 51	43: 51	44: 51	45: 51
46: 51	47: 51				

There are 11 hits at base# 51

HgiAI GWGCWc 20

2: 30	4: 30	6: 30	7: 30	9: 30	10: 30
12: 89	13: 89	14: 89	37: 51	38: 51	39: 51
40: 51	41: 51	42: 51	43: 51	44: 51	45: 51
46: 51	47: 51				

There are 11 hits at base# 51

BsoFI GCngc 26

2: 53	3: 53	5: 53	6: 53	7: 53	8: 53
8: 91	9: 53	10: 53	11: 53	31: 53	36: 36
37: 64	39: 64	40: 64	41: 64	42: 64	43: 64
44: 64	45: 64	46: 64	47: 64	48: 53	49: 53
50: 45	51: 53				

There are 13 hits at base# 53

There are 10 hits at base# 64

TseI Gcwgc 17

2: 53	3: 53	5: 53	6: 53	7: 53	8: 53
9: 53	10: 53	11: 53	31: 53	36: 36	45: 64
46: 64	48: 53	49: 53	50: 45	51: 53	

There are 13 hits at base# 53

MnlI gagg 34

3: 67	3: 95	4: 51	5: 16	5: 67	6: 67
7: 67	8: 67	9: 67	10: 67	11: 67	15: 67
16: 67	17: 67	19: 67	20: 67	21: 67	22: 67
23: 67	24: 67	25: 67	26: 67	27: 67	28: 67
29: 67	30: 67	31: 67	32: 67	33: 67	34: 67
35: 67	36: 67	50: 67	51: 67		

There are 31 hits at base# 67

HpyCH4V TGca 34

5: 90	6: 90	11: 90	12: 90	13: 90	14: 90
15: 44	16: 44	16: 90	17: 44	18: 90	19: 44
20: 44	21: 44	22: 44	23: 44	24: 44	25: 44
26: 44	27: 44	27: 90	28: 44	29: 44	33: 44
34: 44	35: 44	35: 90	36: 38	48: 44	49: 44
50: 44	50: 90	51: 44	51: 52		

There are 21 hits at base# 44

There are 1 hits at base# 52

AccI GTmkac 13 5-base recognition

7: 37	11: 24	37: 16	38: 16	39: 16	40: 16
41: 16	42: 16	43: 16	44: 16	45: 16	46: 16
47: 16					

There are 11 hits at base# 16

SacII CCGCgg 8 6-base recognition

9: 14	10: 14	11: 14	37: 65	39: 65	40: 65
42: 65	43: 65				

There are 5 hits at base# 65

There are 3 hits at base# 14

TfiI Gawtc 24

9: 22	15: 2	16: 2	17: 2	18: 2	19: 2
19: 22	20: 2	21: 2	23: 2	24: 2	25: 2
26: 2	27: 2	28: 2	29: 2	30: 2	31: 2
32: 2	33: 2	33: 22	34: 22	35: 2	36: 2

There are 20 hits at base# 2

BsmAI Nnnnnngagac (SEQ ID NO:88) 19

15: 11 16: 11 20: 11 21: 11 22: 11 23: 11  
24: 11 25: 11 26: 11 27: 11 28: 11 28: 56  
30: 11 31: 11 32: 11 35: 11 36: 11 44: 87  
48: 87

There are 16 hits at base# 11

BpmI ctccag 19

15: 12 16: 12 17: 12 18: 12 20: 12 21: 12  
22: 12 23: 12 24: 12 25: 12 26: 12 27: 12  
28: 12 30: 12 31: 12 32: 12 34: 12 35: 12  
36: 12

There are 19 hits at base# 12

XmnI GAANNnnttc (SEQ ID NO:89) 12

37: 30 38: 30 39: 30 40: 30 41: 30 42: 30  
43: 30 44: 30 45: 30 46: 30 47: 30 50: 30

There are 12 hits at base# 30

BsrI NCcagt 12

37: 32 38: 32 39: 32 40: 32 41: 32 42: 32  
43: 32 44: 32 45: 32 46: 32 47: 32 50: 32

There are 12 hits at base# 32

BanII GRGCYc 11

37: 51 38: 51 39: 51 40: 51 41: 51 42: 51  
43: 51 44: 51 45: 51 46: 51 47: 51

There are 11 hits at base# 51

Ecl136I GAGctc 11

37: 51 38: 51 39: 51 40: 51 41: 51 42: 51  
43: 51 44: 51 45: 51 46: 51 47: 51

There are 11 hits at base# 51

SacI GAGCTc 11

37: 51 38: 51 39: 51 40: 51 41: 51 42: 51  
43: 51 44: 51 45: 51 46: 51 47: 51

There are 11 hits at base# 51

Please delete Table 3 and replace it with the following table:

Table 3: Synthetic 3-23 FR3 of human heavy chains showing positions of possible cleavage sites

```

! Sites engineered into the synthetic gene are shown in upper case DNA
! with the RE name between vertical bars (as in | XbaI |).
! RERSs frequently found in GLGs are shown below the synthetic sequence
! with the name to the right (as in gtn ac=MaeIII(24), indicating that
! 24 of the 51 GLGs contain the site).
!
!
!                                     |---FR3---
!                                     89  90 (codon # in
!                                     R   F  synthetic 3-23)
!                                     |cgc|ttc|  6
! Allowed DNA                       |cgn|tty|
!                                     |agr|
!                                     ga ntc = HinfI(38)
!                                     ga gtc = PheI(18)
!                                     ga wtc = TfiI(20)
!                                     gtn ac = MaeIII(24)
!                                     gts ac = Tsp45I(21)
!                                     tc acc = HphI(44)
!
! -----FR3-----
!      91  92  93  94  95  96  97  98  99 100 101 102 103 104 105
!      T   I   S   R   D   N   S   K   N   T   L   Y   L   Q   M
!
! (SEQ ID NO: 91)
!      |act|atc|TCT|AGA|gac|aac|tct|aag|aat|act|ctc|tac|ttg|cag|atg|  51
! allowed|acn|ath|tcn|cgn|gay|aay|tcn|aar|aay|acn|ttr|tay|ttr|car|atg|
!
! (SEQ ID NO: 90)
!      |agy|agr|          |agy|          |ctn|  |ctn|
!      |      ga|gac = BsmAI(16)          ag ct = AluI(23)
!      c|tcc ag = BpmI(19)          g ctn agc = BlpI(21)
!      |      |          g aan nnn ttc = XmnI(12)
!      | XbaI |          tg ca = HpyCH4V(21)
!
!      ---FR3----->|
!      106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
!      N   S   L   R   A   E   D   T   A   V   Y   Y   C   A   K
!      |aac|agC|TTA|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat|tgc|gct|aaa|  96
! allowed|aay|tcn|ttr|cgn|gcn|gar|gay|acn|gcn|gtn|tay|tay|tgy|gcn|aar|
!      |agy|ctn|agr|          |      |

```

!			cc nng g = BsaJI(23)	ac ngt = Bst4CI(51)
!			aga tct = BglIII(10)	ac ngt = HpyCH4III(51)
!			Rga tcY = BstYI(11)	ac ngt = TaaI(51)
!			c ayn nnn rtc = MslI(44)	
!			cg ryc g = BsiEI(23)	
!			yg gcc r = EaeI(23)	
!			cg gcc g = EagI(23)	
!			g gcc = HaeIII(25)	
!			gag g = MnlI(31)	
!			AflIII	PstI

Please delete Table 4 and replace it with the following table:

Table 4: REdaptors, Extenders, and Bridges used for Cleavage and Capture of Human Heavy Chains in FR3.

**A: HpyCH4V Probes of actual human HC genes (SEQ ID NOS 92-100, respectively, in order of appearance)**

!HpyCH4V in FR3 of human HC, bases 35-56; only those with TGca site TGca;10,

RE recognition:tgca	of length 4 is expected at 10
1	6-1 agttctccctgcagctgaactc
2	3-11,3-07,3-21,3-72,3-48 cactgtatctgcaaatgaacag
3	3-09,3-43,3-20 ccctgtatctgcaaatgaacag
4	5-51 ccgcctacctgcagtggagcag
5	3-15,3-30,3-30.5,3-30.3,3-74,3-23,3-33 cgctgtatctgcaaatgaacag
6	7-4.1 cggcatatctgcagatctgcag
7	3-73 cggcgtatctgcaaatgaacag
8	5-a ctgcctacctgcagtggagcag
9	3-49 tcgcctatctgcaaatgaacag

**B: HpyCH4V REdaptors, Extenders, and Bridges**

**B.1 REdaptors**

! Cutting HC lower strand:

! TmKeller for 100 mM NaCl, zero formamide

! Edaptors for cleavage

		$T_m^W$	$T_m^K$	<u>SEQ</u> <u>ID NO:</u>
(ON_HCFR36-1)	5'-agttctcccTGCAgctgaactc-3'	68.0	64.5	<u>92</u>
(ON_HCFR36-1A)	5'-ttctcccTGCAgctgaactc-3'	62.0	62.5	<u>residues</u> <u>3-22 of 92</u>

(ON\_HCFR36-1B) 5'-ttctcccTGCAgctgaac-3' 56.0 59.9 residues  
3-20 of 92

(ON\_HCFR33-15) 5'-cgctgtatcTGCAaatgaacag-3' 64.0 60.8 96

(ON\_HCFR33-15A) 5'-ctgtatcTGCAaatgaacag-3' 56.0 56.3 residues  
3-22 of 96

(ON\_HCFR33-15B) 5'-ctgtatcTGCAaatgaac-3' 50.0 53.1 residues  
3-20 of 96

(ON\_HCFR33-11) 5'-cactgtatcTGCAaatgaacag-3' 62.0 58.9 93

(ON\_HCFR35-51) 5'-ccgcctaccTGCAgtggagcag-3' 74.0 70.1 95

!

**B.2 Segment of synthetic 3-23 gene into which captured CDR3 is to be cloned**

! XbaI... (SEQ ID NO: 101)

!D323\* cgCttcacTaag tcT aga gac aaC tcT aag aaT acT ctC taC

! scab..... designed gene 3-23 gene.....

!

! HpyCH4V

! .. .. AflIII...

! Ttg caG atg aac agc TtA agG . . .

! ..... . . .

!

### **B.3 Extender and Bridges**

! Extender (bottom strand):

! (SEQ ID NO: 102)

(ON\_HCHpyEx01) 5'-cAAGTAGAgAgTATTcTTAgAgTTgTcTcTAGAcTTAgTgAAgcg-3'

! ON\_HCHpyEx01 is the reverse complement of

! 5'-cgCttcacTaag tcT aga gac aaC tcT aag aaT acT ctC taC Ttg -3'

!

! Bridges (top strand, 9-base overlap):

! (SEQ ID NO: 103)

(ON\_HCHpyBr016-1) 5'-cgCttcacTaag tcT aga gac aaC tcT aag-  
aaT acT ctC taC Ttg CAgctgaac-3' {3'-term C is blocked}

!

! 3-15 et al. + 3-11

(SEQ ID NO: 104)

(ON\_HCHpyBr023-15) 5'-cgCttcacTaag tcT aga gac aaC tcT aag-

aaT acT ctC taC Ttg CAaatgaac-3' {3'-term C is blocked}  
!

! 5-51 (SEQ ID NO: 105)  
(ON\_HCHpyBr045-51) 5'-cgCttcacTaag tcT aga gac aaC tcT aag-  
aaT acT ctC taC Ttg CAgtaggagc-3' {3'-term C is blocked}

! PCR primer (top strand)

! (ON\_HCHpyPCR) 5'-cgCttcacTaag tcT aga gac-3' (SEQ ID NO: 106)

---

**C: B1pI Probes from human HC GLGs**

1	1-58,1-03,1-08,1-69,1-24,1-45,1-46,1-f,1-e	acatggaGCTGAGCagcctgag
<u>(SEQ ID NO: 107)</u>		
2	1-02	acatggaGCTGAGCaggctgag
<u>(SEQ ID NO: 108)</u>		
3	1-18	acatggagctgaggagcctgag
<u>(SEQ ID NO: 109)</u>		
4	5-51,5-a	acctgcagtggagcagcctgaa
<u>(SEQ ID NO: 110)</u>		
5	3-15,3-73,3-49,3-72	atctgcaaataaacagcctgaa
<u>(SEQ ID NO: 111)</u>		
6	3303,3-33,3-07,3-11,3-30,3-21,3-23,3305,3-48	atctgcaaataaacagcctgag
<u>(SEQ ID NO: 112)</u>		
7	3-20,3-74,3-09,3-43	atctgcaaataaacagtctgag
<u>(SEQ ID NO: 113)</u>		
8	74.1	atctgcagatctgcagcctaaa
<u>(SEQ ID NO: 114)</u>		
9	3-66,3-13,3-53,3-d	atcttcaaataaacagcctgag
<u>(SEQ ID NO: 115)</u>		
10	3-64	atcttcaaataagggcagcctgag
<u>(SEQ ID NO: 116)</u>		
11	4301,4-28,4302,4-04,4304,4-31,4-34,4-39,4-59,4-61,4-b	ccctgaaGCTGAGCtctgtgac
<u>(SEQ ID NO: 117)</u>		
12	6-1	ccctgcagctgaactctgtgac
<u>(SEQ ID NO: 118)</u>		
13	2-70,2-05	tccttacaatgaccaacatgga
<u>(SEQ ID NO: 119)</u>		
14	2-26	tccttaccatgaccaacatgga
<u>(SEQ ID NO: 120)</u>		

---



## D: BspI REadaptors, Extenders, and Bridges

### D.1 REadaptors

		$T_m^W$	$T_m^K$
	<u>(SEQ ID NO: 121)</u>		
(BlpF3HC1-58)	5'-ac atg gaG CTG AGC agc ctg ag-3'	70	66.4
	<u>(SEQ ID NO: 122)</u>		
(BlpF3HC6-1)	5'-cc ctg aag ctg agc tct gtg ac-3'	70	66.4
! BlpF3HC6-1 matches 4-30.1, not 6-1.			

### D.2 Segment of synthetic 3-23 gene into which captured CDR3 is to be cloned

!  
BspI  
!  
XbaI...  
...  
!D323\* cgCttcacTaag TCT AGA gac aaC tcT aag aaT acT ctC taC Ttg caG atg  
aac  
(SEQ ID NO: 123)!  
!  
AflIII...  
!  
agC TTA AGG

### D.3 Extender and Bridges

! Bridges

(BlpF3Br1) 5'-cgCttcacTcag tcT aga gaT aaC AGT aaA aaT acT TtG-  
taC Ttg caG Ctg a|GC agc ctg-3' (SEQ ID NO: 124)  
(BlpF3Br2) 5'-cgCttcacTcag tcT aga gaT aaC AGT aaA aaT acT TtG-  
taC Ttg caG Ctg a|gc tct gtg-3' (SEQ ID NO: 125)

!  
| lower strand is cut here

! Extender

(BlpF3Ext) 5'-TcAgcTgcAAgTAcAAAgTATTTTAcTgTTATcTcTAgAcTgAgTgAAgcg-3' (SEQ ID NO: 126)

! BlpF3Ext is the reverse complement of:

! 5'-cgCttcacTcag tcT aga gaT aaC AGT aaA aaT acT TtG taC Ttg caG Ctg a-3'

!

(BlpF3PCR) 5'-cgCttcacTcag tcT aga gaT aaC-3' (SEQ ID NO: 127)

---

**E: HpyCH4III** Distinct GLG sequences surrounding site, bases 77-98

1	102#1,118#4,146#7,169#9,1e#10,311#17,353#30,404#37,4301	ccgtgtattactgtgcgagaga
<u>(SEQ ID NO: 128)</u>		
2	103#2,307#15,321#21,3303#24,333#26,348#28,364#31,366#32	ctgtgtattactgtgcgagaga
<u>(SEQ ID NO: 129)</u>		
3	108#3	ccgtgtattactgtgcgagagg
<u>(SEQ ID NO: 130)</u>		
4	124#5,1f#11	ccgtgtattactgtgcaacaga
<u>(SEQ ID NO: 131)</u>		
5	145#6	ccatgtattactgtgcaagata
<u>(SEQ ID NO: 132)</u>		
6	158#8	ccgtgtattactgtgcggcaga
<u>(SEQ ID NO: 133)</u>		
7	205#12	ccacatattactgtgcacacag
<u>(SEQ ID NO: 134)</u>		
8	226#13	ccacatattactgtgcacggat
<u>(SEQ ID NO: 135)</u>		
9	270#14	ccacgtattactgtgcacggat
<u>(SEQ ID NO: 136)</u>		
10	309#16,343#27	ccttgtattactgtgcaaaaga
<u>(SEQ ID NO: 137)</u>		
11	313#18,374#35,61#50	ctgtgtattactgtgcaagaga
<u>(SEQ ID NO: 138)</u>		
12	315#19	ccgtgtattactgtaccacaga
<u>(SEQ ID NO: 139)</u>		
13	320#20	ccttgtatcactgtgcgagaga
<u>(SEQ ID NO: 140)</u>		
14	323#22	ccgtatattactgtgcgaaaga
<u>(SEQ ID NO: 141)</u>		
15	330#23,3305#25	ctgtgtattactgtgcgaaaga
<u>(SEQ ID NO: 142)</u>		
16	349#29	ccgtgtattactgtactagaga
<u>(SEQ ID NO: 143)</u>		
17	372#33	ccgtgtattactgtgctagaga
<u>(SEQ ID NO: 144)</u>		
18	373#34	ccgtgtattactgtactagaca
<u>(SEQ ID NO: 145)</u>		
19	3d#36	ctgtgtattactgtgaagaaaga
<u>(SEQ ID NO: 146)</u>		
20	428#38	ccgtgtattactgtgcgagaaa
<u>(SEQ ID NO: 147)</u>		
21	4302#40,4304#41	ccgtgtattactgtgccagaga
<u>(SEQ ID NO: 148)</u>		
22	439#44	ctgtgtattactgtgcgagaca
<u>(SEQ ID NO: 149)</u>		
23	551#48	ccatgtattactgtgcgagaca
<u>(SEQ ID NO: 150)</u>		
24	5a#49	ccatgtattactgtgcgaga
<u>(SEQ ID NO: 151)</u>		

## F: HpyCH4III REaptors, Extenders, and Bridges

### F.1 REaptors

(SEQ ID NOS 152-159, respectively, in order of appearance)

! ONs for cleavage of HC(lower) in FR3(bases 77-97)

! For cleavage with HpyCH4III, Bst4CI, or TaaI

! cleavage is in lower chain before base 88.

! 77 788 888 888 889 999 999 9

! 78 901 234 567 890 123 456 7

$T_m^W$

$T_m^K$

(H43.77.97.1-02#1)	5'-cc gtg tat tAC TGT gcg aga g-3'	6462.6
(H43.77.97.1-03#2)	5'-ct gtg tat tAC TGT gcg aga g-3'	6260.6
(H43.77.97.108#3)	5'-cc gtg tat tAC TGT gcg aga g-3'	6462.6
(H43.77.97.323#22)	5'-cc gta tat tac tgt gcg aaa g-3'	6058.7
(H43.77.97.330#23)	5'-ct gtg tat tac tgt gcg aaa g-3'	6058.7
(H43.77.97.439#44)	5'-ct gtg tat tac tgt gcg aga c-3'	6260.6
(H43.77.97.551#48)	5'-cc atg tat tac tgt gcg aga c-3'	6260.6
(H43.77.97.5a#49)	5'-cc atg tat tAC TGT gcg aga -3'	5858.3

### F.2 Extender and Bridges

! XbaI and AflIII sites in bridges are bunged

(H43.XABr1) 5'-ggtgtagtga-

|TCT|AGT|gac|aac|tct|aag|aat|act|ctc|tac|ttg|cag|atg|-

|aac|agC|TTt|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat|tgt|gcg|aga-3'

(SEQ ID NO: 160)

(H43.XABr2) 5'-ggtgtagtga-

|TCT|AGT|gac|aac|tct|aag|aat|act|ctc|tac|ttg|cag|atg|-

|aac|agC|TTt|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat|tgt|gcg|aaa-3'

(SEQ ID NO: 161)

(H43.XAExt) 5'-ATAgTAgAcT gcAgTgTccT cAgcccTTAA gcTgTTcATc TgcAAgTAGA-

gAgTATTcTT AgAgTTgTcT cTAgATcAcT AcAcc-3' (SEQ ID NO: 162)

!H43.XAExt is the reverse complement of

! 5'-ggtgtagtga-

! |TCT|AGA|gac|aac|tct|aag|aat|act|ctc|tac|ttg|cag|atg|-

! |aac|agC|TTA|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat|-3'

(H43.XAPCR) 5'-ggtgtagtga |TCT|AGA|gac|aac-3' (SEQ ID NO: 163)

! XbaI and AflIII sites in bridges are bunged

(H43.ABr1) 5'-ggtgtagtga-

|aac|agC|TTt|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat tgt gcg aga-3'  
(SEQ ID NO: 164)

(H43.ABr2) 5'-gggtgtagtga-

|aac|agC|TTt|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat tgt gcg aaa-3'  
(SEQ ID NO: 165)

(H43.AExt) 5'-ATAgTAgAcTgcAgTgTccTcAgccccTTAAgcTgTTTcAcTAcAcc-3'

(SEQ ID NO: 166)

!(H43.AExt) is the reverse complement of 5'-gggtgtagtga-

! |aac|agC|TTA|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat -3' (SEQ ID NO: 167)

(H43.APCR) 5'-gggtgtagtga |aac|agC|TTA|AGg|gct|g-3' (SEQ ID NO: 168)

Please delete Table 5 and replace it with the following table:

Table 5: Analysis of frequency of matching REadaptors in actual V genes

A: HpyCH4V in HC at bases 35-56

Number of mismatches..... Number															
Id	Ntot	0	1	2	3	4	5	6	7	8	9	10	Cut	Id	Probe
1	510	5	11	274	92	61	25	22	11	1	3	5	443	6-1	agttctcccTGCAgctgaactc
2	192	54	42	32	24	15	2	3	10	3	1	6	167	3-11	cactgtatcTGCAaatgaacag
3	58	19	7	17	6	5	1	0	1	0	2	0	54	3-09	ccctgtatcTGCAaatgaacag
4	267	42	33	9	8	8	82	43	22	8	11	1	100	5-51	ccgcctaccTGCAgtggagcag
5	250	111	59	41	24	7	5	1	0	0	2	0	242	3-15	cgctgtatcTGCAaatgaacag
6	7	0	2	0	1	0	0	0	0	0	4	0	3	7-4.1	cggcatatcTGCAgatctgcag
7	7	0	2	2	0	0	2	1	0	0	0	0	4	3-73	cggcgtatcTGCAaatgaacag
8	26	10	4	1	3	1	2	1	3	1	0	0	19	5-a	ctgcctaccTGCAgtggagcag
9	21	8	2	3	1	6	1	0	0	0	0	0	20	3-49	tcgcctatcTGCAaatgaacag
1338	249	162	379	149	103	120	71	47	13	23	12	1052			(SEQ ID NOS 169-177, respectively in order of appearance)
	249	411	790	939		1162	1280	1316							
					1042	1233	1293	1338							

Id	Probe	dotted probe
6-1	agttctcccTGCAgctgaactc	agttctcccTGCAgctgaactc
3-11	cactgtatcTGCAaatgaacag	cac.g.at.....aa.....ag
3-09	ccctgtatcTGCAaatgaacag	ccc.g.at.....aa.....ag
5-51	ccgcctaccTGCAgtggagcag	ccgc..a.....tg..g.ag

3-15 cgctgtatcTGCAaatgaacag c.c.g.at.....aa.....ag  
7-4.1 cggcatatcTGCAgatctgcag c.gca.at.....a.ctg.ag  
3-73 cggcgtatcTGCAaatgaacag c.gcg.at.....aa.....ag  
5-a ctgcctaccTGCAgtggagcag ctgc..a.....tg..g.ag  
3-49 tcgcctatcTGCAaatgaacag tcgc..at.....aa.....ag

**(SEQ ID NOS 169-177, respectively in order of appearance)**

Seqs with the expected RE site only.....1004

(Counts only cases with 4 or fewer mismatches)

Seqs with only an unexpected site..... 0

Seqs with both expected and unexpected.... 48

(Counts only cases with 4 or fewer mismatches)

Seqs with no sites..... 0

B: B1pl in HC

Id	Ntot	0	1	2	3	4	5	6	7	8	Ncut	Name
1	133	73	16	11	13	6	9	1	4	0	119	1-58 acatggaGCTGAGCagcctgag
2	14	11	1	0	0	0	0	1	0	1	12	1-02 acatggagctgagcaggctgag
3	34	17	8	2	6	1	0	0	0	0	0	1-18 acatggagctgaggagcctgag
4	120	50	32	16	10	9	1	1	1	0	2	5-51 acctgcagtggagcagcctgaa
5	55	13	11	10	17	3	1	0	0	0	0	3-15 atctgcaaatgaacagcctgaa
6	340	186	88	41	15	6	3	0	1	0	0	3303 atctgcaaatgaacagcctgag
7	82	25	16	25	12	1	3	0	0	0	0	3-20 atctgcaaatgaacagtctgag
8	3	0	2	0	1	0	0	0	0	0	0	74.1 atctgcagatctgcagcctaaa
9	23	18	2	2	1	0	0	0	0	0	0	3-66 atcttcaaatgaacagcctgag
10	2	1	0	1	0	0	0	0	0	0	0	3-64 atcttcaaatgggagcctgag

11	486	249	78	81	38	21	10	4	4	1	467	4301	ccctgaagctgagctctgtgac
12	16	6	3	1	0	1	1	3	1	0	1	6-1	ccctgcagctgaactctgtgac
13	28	15	8	2	2	1	0	0	0	0	0	2-70	tccttacaatgaccaacatgga
14	2	0	2	0	0	0	0	0	0	0	0	2-26	tccttaccatgaccaacatgga

(SEQ ID NOS 178-191), respectively

in order of appearance)

601

Name	Full sequence	Dot mode
1-58	acatggaGCTGAGCagcctgag	acatggaGCTGAGCagcctgag
1-02	acatggagctgagcaggctgag	.....g.....
1-18	acatggagctgaggagcctgag	.....g.....
5-51	acctgcagtgagcagcctgaa	..c..c..tg.....a
3-15	atctgcaaatgaacagcctgaa	.tc..c.aa...a.....a
3-30.3	atctgcaaatgaacagcctgag	.tc..c.aa...a.....
3-20	atctgcaaatgaacagtctgag	.tc..c.aa...a...t.....
7-4.1	atctgcagatctgcagcctaaa	.tc..c..a.ct.....a.a
3-66	atcttcaaatgaacagcctgag	.tc.tc.aa...a.....
3-64	atcttcaaatgggcagcctgag	.tc.tc.aa..g.....
4-30.1	ccctgaagctgagctctgtgac	c.c..a.....tctg...c
6-1	ccctgcagctgaactctgtgac	c.c..c.....a.tctg...c
2-70	tccttacaatgaccaacatgga	t.c.tacaa...c..a..ga
2-26	tccttaccatgaccaacatgga	t.c.tacca...c..a..ga

(SEQ ID NOS 178-191, respectively in order of appearance)

Seqs with the expected RE site only..... 597 (counting sequences with 4 or fewer mismatches)

Seqs with only an unexpected site..... 2

Seqs with both expected and unexpected.... 2





in order of appearance)

Cumulative	337	808	1171	1389	1519	1577	1600	1611	1617
Seqs with the expected RE site only.....	1511								
Seqs with only an unexpected site.....	0								
Seqs with both expected and unexpected....	8								
Seqs with no sites.....	0								

Please delete Table 5D and replace it with the following table:

Table 5D:

Analysis repeated using only 8 best REaptors

Id	Ntot	0	1	2	3	4	5	6	7	8+	
1	301	78	101	54	32	16	9	10	1	0	281 102#1
ccgtgtattactgtgcgagaga (SEQ ID NO: 267)											
2	493	69	155	125	73	37	14	11	3	6	459 103#2
ctgtgtattactgtgcgagaga (SEQ ID NO: 268)											
3	189	52	45	38	23	18	5	4	1	3	176 108#3
ccgtgtattactgtgcgagagg (SEQ ID NO: 269)											
4	127	29	23	28	24	10	6	5	2	0	114 323#22
ccgtatattactgtgcgaaaga (SEQ ID NO: 270)											
5	78	21	25	14	11	1	4	2	0	0	72 330#23
ctgtgtattactgtgcgaaaga 6 79 15 17 25 8 11 1 2 0 0											
76	439#44	ctgtgtattactgtgcgagaca (SEQ ID NO: 272)									
7	43	14	15	5	5	3	0	1	0	0	42 551#48
ccatgtattactgtgcgagaca (SEQ ID NO: 273)											
8	307	26	63	72	51	38	24	14	13	6	250 5a#49
ccatgtattactgtgcgaga (residues 1-20 of SEQ ID NO: 274)											
1	102#1	ccgtgtattactgtgcgagaga ccgtgtattactgtgcgagaga									
2	103#2	ctgtgtattactgtgcgagaga .t.....									
3	108#3	ccgtgtattactgtgcgagagg .....g									
4	323#22	ccgtatattactgtgcgaaaga ....a.....a...									
5	330#23	ctgtgtattactgtgcgaaaga .t.....a...									
6	439#44	ctgtgtattactgtgcgagaca .t.....c.									
7	551#48	ccatgtattactgtgcgagaca ..a.....c.									
8	5a#49	ccatgtattactgtgcgagaAA ..a.....AA									
(SEQ ID NOS 267-274, respectively in order of appearance)											
Seqs with the expected RE site only.....1463 / 1617											
Seqs with only an unexpected site..... 0											
Seqs with both expected and unexpected.... 7											
Seqs with no sites..... 0											

Please delete Table 6 and replace it with the following table:

Table 6: Human HC GLG FR1 Sequences

VH Exon - Nucleotide sequence alignment

VH1

1-02	CAG GTG CAG CTG GTG CAG TCT GGG GCT GAG GTG AAG AAG CCT GGG GCC TCA GTG AAG GTC TCC TGC AAG GCT TCT GGA TAC ACC TTC ACC <u>(SEQ ID NO: 216)</u>
1-03	cag gtC cag ctT gtg cag tct ggg gct gag gtg aag aag cct ggg gcc tca gtg aag gtT tcc tgc aag gct tct gga tac acc ttc acT <u>(SEQ ID NO: 217)</u>
1-08	cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag cct ggg gcc tca gtg aag gtc tcc tgc aag gct tct gga tac acc ttc acc <u>(SEQ ID NO: 218)</u>
1-18	cag gtT cag ctg gtg cag tct ggA gct gag gtg aag aag cct ggg gcc tca gtg aag gtc tcc tgc aag gct tct ggT tac acc ttT acc <u>(SEQ ID NO: 219)</u>
1-24	cag gtC cag ctg gtA cag tct ggg gct gag gtg aag aag cct ggg gcc tca gtg aag gtc tcc tgc aag gTt tCc gga tac acc Ctc acT <u>(SEQ ID NO: 220)</u>
1-45	cag Atg cag ctg gtg cag tct ggg gct gag gtg aag aag Act ggg Tcc tca gtg aag gtT tcc tgc aag gct tCc gga tac acc ttc acc <u>(SEQ ID NO: 221)</u>
1-46	cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag cct ggg gcc tca gtg aag gtT tcc tgc aag gcA tct gga tac acc ttc acc <u>(SEQ ID NO: 222)</u>
1-58	caA Atg cag ctg gtg cag tct ggg Cct gag gtg aag aag cct ggg Acc tca gtg aag gtc tcc tgc aag gct tct gga tTc acc ttT acT <u>(SEQ ID NO: 223)</u>
1-69	cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag cct ggg Tcc tCg gtg aag gtc tcc tgc aag gct tct gga GGc acc ttc aGc <u>(SEQ ID NO: 224)</u>
1-e	cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag cct ggg Tcc tCg gtg aag gtc tcc tgc aag gct tct gga GGc acc ttc aGc <u>(SEQ ID NO: 225)</u>
1-f	Gag gtC cag ctg gtA cag tct ggg gct gag gtg aag aag cct ggg gCT Aca gtg aaA Atc tcc tgc aag gTt tct gga tac acc ttc acc <u>(SEQ ID NO: 226)</u>

VH2

2-05	CAG ATC ACC TTG AAG GAG TCT GGT CCT ACG CTG GTG AAA CCC ACA CAG ACC CTC ACG CTG ACC TGC ACC TTC TCT GGG TTC TCA CTC AGC <u>(SEQ ID NO: 227)</u>
2-26	cag Gtc acc ttg aag gag tct ggt cct GTg ctg gtg aaa ccc aca Gag acc ctc acg ctg acc tgc acc Gtc tct ggg ttc tca ctc agc <u>(SEQ ID NO: 228)</u>
2-70	cag Gtc acc ttg aag gag tct ggt cct Gcg ctg gtg aaa ccc aca cag acc ctc acA ctg acc tgc acc ttc tct ggg ttc tca ctc agc <u>(SEQ ID NO: 229)</u>

VH3

3-07	GAG GTG CAG CTG GTG GAG TCT GGG GGA GGC TTG GTC CAG CCT GGG GGG TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTT AGT <u>(SEQ ID NO: 230)</u>
3-09	gaA gtg cag ctg gtg gag tct ggg gga ggc ttg gtA cag cct ggC Agg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt Gat <u>(SEQ ID NO: 231)</u>
3-11	Cag gtg cag ctg gtg gag tct ggg gga ggc ttg gtc Aag cct ggA ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttC agt <u>(SEQ ID NO: 232)</u>
3-13	gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtA cag cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttC agt <u>(SEQ ID NO: 233)</u>

3-15 gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtA Aag cct ggg ggg tcc ctT aga  
ctc tcc tgt gca gcc tct gga ttc acT ttC agt (SEQ ID NO: 234)

3-20 gag gtg cag ctg gtg gag tct ggg gga ggT Gtg gtA cGg cct ggg ggg tcc ctg aga  
ctc tcc tgt gca gcc tct gga ttc acc ttt Gat (SEQ ID NO: 235)

3-21 gag gtg cag ctg gtg gag tct ggg gga ggc Ctg gtc Aag cct ggg ggg tcc ctg aga  
ctc tcc tgt gca gcc tct gga ttc acc ttC agt (SEQ ID NO: 236)

3-23 gag gtg cag ctg Ttg gag tct ggg gga ggc ttg gtA cag cct ggg ggg tcc ctg aga  
ctc tcc tgt gca gcc tct gga ttc acc ttt agC (SEQ ID NO: 237)

3-30 Cag gtg cag ctg gtg gag tct ggg gga ggc Gtg gtc cag cct ggg Agg tcc ctg aga  
ctc tcc tgt gca gcc tct gga ttc acc ttC agt (SEQ ID NO: 238)

3-30.3 Cag gtg cag ctg gtg gag tct ggg gga ggc Gtg gtc cag cct ggg Agg tcc ctg aga  
ctc tcc tgt gca gcc tct gga ttc acc ttC agt (SEQ ID NO: 239)

3-30.5 Cag gtg cag ctg gtg gag tct ggg gga ggc Gtg gtc cag cct ggg Agg tcc ctg aga  
ctc tcc tgt gca gcc tct gga ttc acc ttC agt (SEQ ID NO: 240)

3-33 Cag gtg cag ctg gtg gag tct ggg gga ggc Gtg gtc cag cct ggg Agg tcc ctg aga  
ctc tcc tgt gca gcG tct gga ttc acc ttC agt (SEQ ID NO: 241)

3-43 gaA gtg cag ctg gtg gag tct ggg gga gTc Gtg gtA cag cct ggg ggg tcc ctg aga  
ctc tcc tgt gca gcc tct gga ttc acc ttt Gat (SEQ ID NO: 242)

3-48 gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtA cag cct ggg ggg tcc ctg aga  
ctc tcc tgt gca gcc tct gga ttc acc ttC agt (SEQ ID NO: 243)

3-49 gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtA cag ccA ggg Cgg tcc ctg aga  
ctc tcc tgt Aca gcT tct gga ttc acc ttt Ggt (SEQ ID NO: 244)

3-53 gag gtg cag ctg gtg gag Act ggA gga ggc ttg Atc cag cct ggg ggg tcc ctg aga  
ctc tcc tgt gca gcc tct ggG ttc acc GtC agt (SEQ ID NO: 245)

3-64 gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtc cag cct ggg ggg tcc ctg aga  
ctc tcc tgt gca gcc tct gga ttc acc ttC agt (SEQ ID NO: 246)

3-66 gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtc cag cct ggg ggg tcc ctg aga  
ctc tcc tgt gca gcc tct gga ttc acc GtC agt (SEQ ID NO: 247)

3-72 gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtc cag cct ggA ggg tcc ctg aga  
ctc tcc tgt gca gcc tct gga ttc acc ttC agt (SEQ ID NO: 248)

3-73 gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtc cag cct ggg ggg tcc ctg aAa  
ctc tcc tgt gca gcc tct ggG ttc acc ttC agt (SEQ ID NO: 249)

3-74 gag gtg cag ctg gtg gag tcC ggg gga ggc ttA gtT cag cct ggg ggg tcc ctg aga  
ctc tcc tgt gca gcc tct gga ttc acc ttC agt (SEQ ID NO: 250)

3-d gag gtg cag ctg gtg gag tct Cgg gga gTc ttg gtA cag cct ggg ggg tcc ctg aga  
ctc tcc tgt gca gcc tct gga ttc acc GtC agt (SEQ ID NO: 251)

VH4

4-04 CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG CCT TCG GGG ACC CTG TCC  
CTC ACC TGC GCT GTC TCT GGT GGC TCC ATC AGC (SEQ ID NO: 252)

4-28 cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg gAC acc ctg tcc  
ctc acc tgc gct gtc tct ggt TAc tcc atc agc (SEQ ID NO: 253)

4-30.1 cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcA CAg acc ctg tcc  
ctc acc tgc Act gtc tct ggt ggc tcc atc agc (SEQ ID NO: 254)

4-30.2 cag Ctg cag ctg cag gag tcC ggc Tca gga ctg gtg aag cct tcA CAg acc ctg tcc  
ctc acc tgc gct gtc tct ggt ggc tcc atc agc (SEQ ID NO: 255)

4-30.4 cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcA CAg acc ctg tcc  
ctc acc tgc Act gtc tct ggt ggc tcc atc agc (SEQ ID NO: 256)

4-31 cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcA CAg acc ctg tcc  
ctc acc tgc Act gtc tct ggt ggc tcc atc agc (SEQ ID NO: 257)

4-34 cag gtg cag ctA cag Cag tGg ggc Gca gga ctg Ttg aag cct tcg gAg acc ctg tcc  
ctc acc tgc gct gtc tAt ggt ggG tcc Ttc agT (SEQ ID NO: 258)

4-39 cag Ctg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg gAg acc ctg tcc  
ctc acc tgc Act gtc tct ggt ggc tcc atc agc (SEQ ID NO: 259)

4-59 cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg gAg acc ctg tcc  
ctc acc tgc Act gtc tct ggt ggc tcc atc agT (SEQ ID NO: 260)

4-61 cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg gAg acc ctg tcc  
ctc acc tgc Act gtc tct ggt ggc tcc Gtc agc (SEQ ID NO: 261)

4-b cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg gAg acc ctg tcc  
ctc acc tgc gct gtc tct ggt TAc tcc atc agc (SEQ ID NO: 262)

VH5

5-51 GAG GTG CAG CTG GTG CAG TCT GGA GCA GAG GTG AAA AAG CCC GGG GAG TCT CTG AAG  
ATC TCC TGT AAG GGT TCT GGA TAC AGC TTT ACC (SEQ ID NO: 263)

5-a gaA gtg cag ctg gtg cag tct gga gca gag gtg aaa aag ccc ggg gag tct ctg aGg  
atc tcc tgt aag ggt tct gga tac agc ttt acc (SEQ ID NO: 264)

VH6

6-1 CAG GTA CAG CTG CAG CAG TCA GGT CCA GGA CTG GTG AAG CCC TCG CAG ACC CTC TCA  
CTC ACC TGT GCC ATC TCC GGG GAC AGT GTC TCT (SEQ ID NO: 265)

VH7

7-4.1 CAG GTG CAG CTG GTG CAA TCT GGG TCT GAG TTG AAG AAG CCT GGG GCC TCA GTG AAG  
GTT TCC TGC AAG GCT TCT GGA TAC ACC TTC ACT (SEQ ID NO: 266)

Please delete Table 7 and replace it with the following table:

Table 7: RERS sites in Human HC GLG FR1s where there are at least 20 GLGs cut

BsgI GTGCAG			71 (cuts 16/14 bases to right)		
1: 4	1: 13	2: 13	3: 4	3: 13	4: 13
6: 13	7: 4	7: 13	8: 13	9: 4	9: 13
10: 4	10: 13	15: 4	15: 65	16: 4	16: 65
17: 4	17: 65	18: 4	18: 65	19: 4	19: 65
20: 4	20: 65	21: 4	21: 65	22: 4	22: 65
23: 4	23: 65	24: 4	24: 65	25: 4	25: 65
26: 4	26: 65	27: 4	27: 65	28: 4	28: 65
29: 4	30: 4	30: 65	31: 4	31: 65	32: 4
32: 65	33: 4	33: 65	34: 4	34: 65	35: 4
35: 65	36: 4	36: 65	37: 4	38: 4	39: 4
41: 4	42: 4	43: 4	45: 4	46: 4	47: 4
48: 4	48: 13	49: 4	49: 13	51: 4	
<b>There are 39 hits at base# 4</b>					
There are 21 hits at base# 65					

-"- ctgcac			9		
12: 63	13: 63	14: 63	39: 63	41: 63	42: 63
44: 63	45: 63	46: 63			
BbvI GCAGC			65		
1: 6	3: 6	6: 6	7: 6	8: 6	9: 6
10: 6	15: 6	15: 67	16: 6	16: 67	17: 6
17: 67	18: 6	18: 67	19: 6	19: 67	20: 6
20: 67	21: 6	21: 67	22: 6	22: 67	23: 6
23: 67	24: 6	24: 67	25: 6	25: 67	26: 6
26: 67	27: 6	27: 67	28: 6	28: 67	29: 6
30: 6	30: 67	31: 6	31: 67	32: 6	32: 67
33: 6	33: 67	34: 6	34: 67	35: 6	35: 67
36: 6	36: 67	37: 6	38: 6	39: 6	40: 6
41: 6	42: 6	43: 6	44: 6	45: 6	46: 6
47: 6	48: 6	49: 6	50: 12	51: 6	
<b>There are 43 hits at base# 6 Bolded sites very near sites listed below</b>					

There are 21 hits at base# 67

-"- gctgc 13

37: 9 38: 9 39: 9 40: 3 40: 9 41: 9  
42: 9 44: 3 44: 9 45: 9 46: 9 47: 9  
50: 9

There are 11 hits at base# 9

BsoFI GCngc 78

1: 6 3: 6 6: 6 7: 6 8: 6 9: 6  
10: 6 15: 6 15: 67 16: 6 16: 67 17: 6  
17: 67 18: 6 18: 67 19: 6 19: 67 20: 6  
20: 67 21: 6 21: 67 22: 6 22: 67 23: 6  
23: 67 24: 6 24: 67 25: 6 25: 67 26: 6  
26: 67 27: 6 27: 67 28: 6 28: 67 29: 6  
30: 6 30: 67 31: 6 31: 67 32: 6 32: 67  
33: 6 33: 67 34: 6 34: 67 35: 6 35: 67  
36: 6 36: 67 37: 6 37: 9 38: 6 38: 9  
39: 6 39: 9 40: 3 40: 6 40: 9 41: 6  
41: 9 42: 6 42: 9 43: 6 44: 3 44: 6  
44: 9 45: 6 45: 9 46: 6 46: 9 47: 6  
47: 9 48: 6 49: 6 50: 9 50: 12 51: 6

There are 43 hits at base# 6 These often occur together.

There are 11 hits at base# 9

There are 2 hits at base# 3

There are 21 hits at base# 67

TseI GcwgC 78

1: 6 3: 6 6: 6 7: 6 8: 6 9: 6  
10: 6 15: 6 15: 67 16: 6 16: 67 17: 6  
17: 67 18: 6 18: 67 19: 6 19: 67 20: 6  
20: 67 21: 6 21: 67 22: 6 22: 67 23: 6  
23: 67 24: 6 24: 67 25: 6 25: 67 26: 6  
26: 67 27: 6 27: 67 28: 6 28: 67 29: 6  
30: 6 30: 67 31: 6 31: 67 32: 6 32: 67  
33: 6 33: 67 34: 6 34: 67 35: 6 35: 67  
36: 6 36: 67 37: 6 37: 9 38: 6 38: 9

<u>39: 6</u>	<u>39: 9</u>	<u>40: 3</u>	<u>40: 6</u>	<u>40: 9</u>	<u>41: 6</u>
<u>41: 9</u>	<u>42: 6</u>	<u>42: 9</u>	<u>43: 6</u>	<u>44: 3</u>	<u>44: 6</u>
<u>44: 9</u>	<u>45: 6</u>	<u>45: 9</u>	<u>46: 6</u>	<u>46: 9</u>	<u>47: 6</u>
<u>47: 9</u>	<u>48: 6</u>	<u>49: 6</u>	<u>50: 9</u>	<u>50: 12</u>	<u>51: 6</u>

There are 43 hits at base# 6 Often together.

There are 11 hits at base# 9

There are 2 hits at base# 3

There are 1 hits at base# 12

There are 21 hits at base# 67

MspAII CMGckg

48

1: 7	3: 7	4: 7	5: 7	6: 7	7: 7
8: 7	9: 7	10: 7	11: 7	15: 7	16: 7
17: 7	18: 7	19: 7	20: 7	21: 7	22: 7
23: 7	24: 7	25: 7	26: 7	27: 7	28: 7
29: 7	30: 7	31: 7	32: 7	33: 7	34: 7
35: 7	36: 7	37: 7	38: 7	39: 7	<u>40: 1</u>
<u>40: 7</u>	41: 7	42: 7	<u>44: 1</u>	<u>44: 7</u>	45: 7
46: 7	47: 7	48: 7	49: 7	50: 7	51: 7

There are 46 hits at base# 7

PvuII CAGctg

48

1: 7	3: 7	4: 7	5: 7	6: 7	7: 7
8: 7	9: 7	10: 7	11: 7	15: 7	16: 7
17: 7	18: 7	19: 7	20: 7	21: 7	22: 7
23: 7	24: 7	25: 7	26: 7	27: 7	28: 7
29: 7	30: 7	31: 7	32: 7	33: 7	34: 7
35: 7	36: 7	37: 7	38: 7	39: 7	<u>40: 1</u>
<u>40: 7</u>	41: 7	42: 7	<u>44: 1</u>	<u>44: 7</u>	45: 7
46: 7	47: 7	48: 7	49: 7	50: 7	51: 7

There are 46 hits at base# 7

There are 2 hits at base# 1

AluI AGct

54

1: 8	2: 8	3: 8	4: 8	4: 24	5: 8
------	------	------	------	-------	------



6: 8	7: 8	8: 8	9: 8	10: 8	11: 8
15: 8	16: 8	17: 8	18: 8	19: 8	20: 8
21: 8	22: 8	23: 8	24: 8	25: 8	26: 8
27: 8	28: 8	29: 8	29: 69	30: 8	31: 8
32: 8	33: 8	34: 8	35: 8	36: 8	37: 8
38: 8	39: 8	<u>40: 2</u>	<u>40: 8</u>	41: 8	42: 8
43: 8	<u>44: 2</u>	<u>44: 8</u>	45: 8	46: 8	47: 8
48: 8	48: 82	49: 8	49: 82	50: 8	51: 8

There are 48 hits at base# 8

There are 2 hits at base# 2

DdeI Ctnag

48

1: 26	1: 48	2: 26	2: 48	3: 26	3: 48
4: 26	4: 48	5: 26	5: 48	6: 26	6: 48
7: 26	7: 48	8: 26	8: 48	9: 26	10: 26
11: 26	12: 85	13: 85	14: 85	15: 52	16: 52
17: 52	18: 52	19: 52	20: 52	21: 52	22: 52
23: 52	24: 52	25: 52	26: 52	27: 52	28: 52
29: 52	30: 52	31: 52	32: 52	33: 52	35: 30
35: 52	36: 52	40: 24	49: 52	51: 26	51: 48

There are 22 hits at base# 52 52 and 48 never together.

There are 9 hits at base# 48

There are 12 hits at base# 26 26 and 24 never together.

HphI tcacc

42

1: 86	3: 86	6: 86	7: 86	8: 80	11: 86
12: 5	13: 5	14: 5	15: 80	16: 80	17: 80
18: 80	20: 80	21: 80	22: 80	23: 80	24: 80
25: 80	26: 80	27: 80	28: 80	29: 80	30: 80
31: 80	32: 80	33: 80	34: 80	35: 80	36: 80
37: 59	38: 59	39: 59	40: 59	41: 59	42: 59
43: 59	44: 59	45: 59	46: 59	47: 59	50: 59

There are 22 hits at base# 80 80 and 86 never together

There are 5 hits at base# 86

There are 12 hits at base# 59

BssKI Nccngg

50

1: 39	2: 39	3: 39	4: 39	5: 39	7: 39
8: 39	9: 39	10: 39	11: 39	15: 39	16: 39
17: 39	18: 39	19: 39	20: 39	21: 29	21: 39
22: 39	23: 39	24: 39	25: 39	26: 39	27: 39
28: 39	29: 39	30: 39	31: 39	32: 39	33: 39
34: 39	35: 19	35: 39	36: 39	37: 24	38: 24
39: 24	41: 24	42: 24	44: 24	45: 24	46: 24
47: 24	<u>48: 39</u>	<u>48: 40</u>	<u>49: 39</u>	<u>49: 40</u>	50: 24
50: 73	51: 39				

**There are 35 hits at base# 39 39 and 40 together twice.**

There are 2 hits at base# 40

BsaJI Ccnngg

47

1: 40	2: 40	3: 40	4: 40	5: 40	7: 40
8: 40	9: 40	9: 47	10: 40	10: 47	11: 40
15: 40	18: 40	19: 40	20: 40	21: 40	22: 40
23: 40	24: 40	25: 40	26: 40	27: 40	28: 40
29: 40	30: 40	31: 40	32: 40	34: 40	35: 20
35: 40	36: 40	37: 24	38: 24	39: 24	41: 24
42: 24	44: 24	45: 24	46: 24	47: 24	<u>48: 40</u>
<u>48: 41</u>	<u>49: 40</u>	<u>49: 41</u>	50: 74	51: 40	

**There are 32 hits at base# 40 40 and 41 together twice**

**There are 2 hits at base# 41**

There are 9 hits at base# 24

**There are 2 hits at base# 47**

BstNI CCwgg

44

PspGI ccwgg

ScrFI(\$M.HpaII) CCwgg

1: 40	2: 40	3: 40	4: 40	5: 40	7: 40
8: 40	9: 40	10: 40	11: 40	15: 40	16: 40
17: 40	18: 40	19: 40	20: 40	21: 30	21: 40
22: 40	23: 40	24: 40	25: 40	26: 40	27: 40
28: 40	29: 40	30: 40	31: 40	32: 40	33: 40

34: 40    35: 40    36: 40    37: 25    38: 25    39: 25  
 41: 25    42: 25    44: 25    45: 25    46: 25    47: 25  
 50: 25    51: 40

**There are 33 hits at base# 40**

ScrFI CCngg

50

1: 40    2: 40    3: 40    4: 40    5: 40    7: 40  
 8: 40    9: 40    10: 40    11: 40    15: 40    16: 40  
 17: 40    18: 40    19: 40    20: 40    21: 30    21: 40  
 22: 40    23: 40    24: 40    25: 40    26: 40    27: 40  
 28: 40    29: 40    30: 40    31: 40    32: 40    33: 40  
 34: 40    35: 20    35: 40    36: 40    37: 25    38: 25  
 39: 25    41: 25    42: 25    44: 25    45: 25    46: 25  
  
 47: 25    48: 40    48: 41    49: 40    49: 41    50: 25  
 50: 74    51: 40

**There are 35 hits at base# 40**

**There are 2 hits at base# 41**

EcoO109I RGgnccy

34

1: 43    2: 43    3: 43    4: 43    5: 43    6: 43  
 7: 43    8: 43    9: 43    10: 43    15: 46    16: 46  
 17: 46    18: 46    19: 46    20: 46    21: 46    22: 46  
 23: 46    24: 46    25: 46    26: 46    27: 46    28: 46  
 30: 46    31: 46    32: 46    33: 46    34: 46    35: 46  
 36: 46    37: 46    43: 79    51: 43

**There are 22 hits at base# 46 46 and 43 never together**

**There are 11 hits at base# 43**

NlaIV GGNncc

71

1: 43    2: 43    3: 43    4: 43    5: 43    6: 43  
 7: 43    8: 43    9: 43    9: 79    10: 43    10: 79  
15: 46    15: 47    16: 47    17: 46    17: 47    18: 46  
18: 47    19: 46    19: 47    20: 46    20: 47    21: 46  
21: 47    22: 46    22: 47    23: 47    24: 47    25: 47  
 26: 47    27: 46    27: 47    28: 46    28: 47    29: 47  
30: 46    30: 47    31: 46    31: 47    32: 46    32: 47

<u>33: 46</u>	<u>33: 47</u>	<u>34: 46</u>	<u>34: 47</u>	<u>35: 46</u>	<u>35: 47</u>
<u>36: 46</u>	<u>36: 47</u>	37: 21	<u>37: 46</u>	<u>37: 47</u>	37: 79
38: 21	39: 21	39: 79	40: 79	41: 21	41: 79
42: 21	42: 79	43: 79	44: 21	44: 79	45: 21
45: 79	46: 21	46: 79	47: 21	51: 43	

There are 23 hits at base# 47 46 & 47 often together

There are 17 hits at base# 46 There are 11 hits at base# 43

Sau96I Ggncc

70

1: 44	2: 3	2: 44	3: 44	4: 44	5: 3	5: 44	6:
44							
7: 44	8: 22	8: 44	9: 44	10: 44	11: 3	12: 22	13:
22							
14: 22	15: 33	15: 47	16: 47	17: 47	18: 47	19: 47	20:
47							
21: 47	22: 47	23: 33	23: 47	24: 33	24: 47	25: 33	25:
47							
26: 33	26: 47	27: 47	28: 47	29: 47	30: 47	31: 33	31:
47							
32: 33	32: 47	33: 33	33: 47	34: 33	34: 47	35: 47	36:
47							
<u>37: 21</u>	<u>37: 22</u>	37: 47	<u>38: 21</u>	<u>38: 22</u>	39: 21	39: 22	41:
21							
41: 22	42: 21	42: 22	43: 80	44: 21	44: 22	45: 21	45:
22							
46: 21	46: 22	47: 21	47: 22	50: 22	51: 44		

There are 23 hits at base# 47 These do not occur together.

There are 11 hits at base# 44

There are 14 hits at base# 22 These do occur together.

There are 9 hits at base# 21

(SEQ ID NO: 13)

BsmAI GTCTCNnnnn 22

1: 58	3: 58	4: 58	5: 58	8: 58	9: 58
10: 58	13: 70	36: 18	37: 70	38: 70	39: 70
40: 70	41: 70	42: 70	44: 70	45: 70	46: 70
47: 70	48: 48	49: 48	50: 85		

There are 11 hits at base# 70

(SEQ ID NO: 14)

- "- Nnnnnngagac 27

13: 40	15: 48	16: 48	17: 48	18: 48	20: 48
21: 48	22: 48	23: 48	24: 48	25: 48	26: 48
27: 48	28: 48	29: 48	30: 10	30: 48	31: 48
32: 48	33: 48	35: 48	36: 48	43: 40	44: 40
45: 40	46: 40	47: 40			

There are 20 hits at base# 48

AvaII Ggwcc 44

Sau96I(\$M.HaeIII) Ggwcc 44

2: 3	5: 3	6: 44	8: 44	9: 44	10: 44
11: 3	12: 22	13: 22	14: 22	15: 33	15: 47
16: 47	17: 47	18: 47	19: 47	20: 47	21: 47
22: 47	23: 33	23: 47	24: 33	24: 47	25: 33
25: 47	26: 33	26: 47	27: 47	28: 47	29: 47
30: 47	31: 33	31: 47	32: 33	32: 47	33: 33
33: 47	34: 33	34: 47	35: 47	36: 47	37: 47
43: 80	50: 22				

There are 23 hits at base# 47 44 & 47 never together

There are 4 hits at base# 44

PpuMI RGgwccy 27

6: 43	8: 43	9: 43	10: 43	15: 46	16: 46
17: 46	18: 46	19: 46	20: 46	21: 46	22: 46
23: 46	24: 46	25: 46	26: 46	27: 46	28: 46
30: 46	31: 46	32: 46	33: 46	34: 46	35: 46
36: 46	37: 46	43: 79			

There are 22 hits at base# 46 43 and 46 never occur together.

There are 4 hits at base# 43

BsmFI GGGAC

3

8: 43 37: 46 50: 77

-"- gtccc

33

15: 48 16: 48 17: 48 1: 0 1: 0 20: 48

21: 48 22: 48 23: 48 24: 48 25: 48 26: 48

27: 48 28: 48 29: 48 30: 48 31: 48 32: 48

33: 48 34: 48 35: 48 36: 48 37: 54 38: 54

39: 54 40: 54 41: 54 42: 54 43: 54 44: 54

45: 54 46: 54 47: 54

There are 20 hits at base# 48

There are 11 hits at base# 54

HinfI Gantc

80

8: 77 12: 16 13: 16 14: 16 15: 16 15: 56

15: 77 16: 16 16: 56 16: 77 17: 16 17: 56

17: 77 18: 16 18: 56 18: 77 19: 16 19: 56

19: 77 20: 16 20: 56 20: 77 21: 16 21: 56

21: 77 22: 16 22: 56 22: 77 23: 16 23: 56

23: 77 24: 16 24: 56 24: 77 25: 16 25: 56

25: 77 26: 16 26: 56 26: 77 27: 16 27: 26

27: 56 27: 77 28: 16 28: 56 28: 77 29: 16

29: 56 29: 77 30: 56 31: 16 31: 56 31: 77

32: 16 32: 56 32: 77 33: 16 33: 56 33: 77

34: 16 35: 16 35: 56 35: 77 36: 16 36: 26

36: 56 36: 77 37: 16 38: 16 39: 16 40: 16

41: 16 42: 16 44: 16 45: 16 46: 16 47: 16

48: 46 49: 46

There are 34 hits at base# 16

TfiI Gawtc

21

8: 77 15: 77 16: 77 17: 77 18: 77 19: 77

20: 77 21: 77 22: 77 23: 77 24: 77 25: 77



AlwNI CAGNNNctg

26

15: 68 16: 68 17: 68 18: 68 19: 68 20: 68

21: 68 22: 68 23: 68 24: 68 25: 68 26: 68

27: 68 28: 68 29: 68 30: 68 31: 68 32: 68

33: 68 34: 68 35: 68 36: 68 39: 46 40: 46

41: 46 42: 46

There are 22 hits at base# 68

Please delete Table 8 and replace it with the following table:

Table 8: Kappa FR1 GLGs

!	1	2	3	4	5	6	7	8	9	10	11	12	
	GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	
!	13	14	15	16	17	18	19	20	21	22	23		
	GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGC	!	O12( <u>SEQ ID NO: 275</u> )
	GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	
	GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGC	!	O2( <u>SEQ ID NO: 276</u> )
	GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	
	GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGC	!	O18( <u>SEQ ID NO: 277</u> )
	GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	
	GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGC	!	O8( <u>SEQ ID NO: 278</u> )
	GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	
	GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGC	!	A20( <u>SEQ ID NO: 279</u> )
	GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	
	GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGC	!	A30( <u>SEQ ID NO: 280</u> )
	AAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCT	GCC	ATG	TCT	
	GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGT	!	L14( <u>SEQ ID NO: 281</u> )
	GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCC	TCA	CTG	TCT	
	GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGT	!	L1( <u>SEQ ID NO: 282</u> )
	GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCC	TCA	CTG	TCT	
	GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGT	!	L15( <u>SEQ ID NO: 283</u> )
	GCC	ATC	CAG	TTG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	
	GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGC	!	L4( <u>SEQ ID NO: 284</u> )
	GCC	ATC	CAG	TTG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	



GCA TCT GTA GGA GAC AGA GTC ACC ATC ACT TGC ! L18(SEQ ID NO: 285)  
GAC ATC CAG ATG ACC CAG TCT CCA TCT TCC GTG TCT  
GCA TCT GTA GGA GAC AGA GTC ACC ATC ACT TGT ! L5(SEQ ID NO: 286)  
GAC ATC CAG ATG ACC CAG TCT CCA TCT TCT GTG TCT  
GCA TCT GTA GGA GAC AGA GTC ACC ATC ACT TGT ! L19(SEQ ID NO: 287)  
GAC ATC CAG TTG ACC CAG TCT CCA TCC TTC CTG TCT  
GCA TCT GTA GGA GAC AGA GTC ACC ATC ACT TGC ! L8(SEQ ID NO: 288)  
GCC ATC CGG ATG ACC CAG TCT CCA TTC TCC CTG TCT  
GCA TCT GTA GGA GAC AGA GTC ACC ATC ACT TGC ! L23(SEQ ID NO: 289)  
GCC ATC CGG ATG ACC CAG TCT CCA TCC TCA TTC TCT  
GCA TCT ACA GGA GAC AGA GTC ACC ATC ACT TGT ! L9(SEQ ID NO: 290)  
GTC ATC TGG ATG ACC CAG TCT CCA TCC TTA CTC TCT  
GCA TCT ACA GGA GAC AGA GTC ACC ATC AGT TGT ! L24(SEQ ID NO: 291)  
GCC ATC CAG ATG ACC CAG TCT CCA TCC TCC CTG TCT  
GCA TCT GTA GGA GAC AGA GTC ACC ATC ACT TGC ! L11(SEQ ID NO: 292)  
GAC ATC CAG ATG ACC CAG TCT CCT TCC ACC CTG TCT  
GCA TCT GTA GGA GAC AGA GTC ACC ATC ACT TGC ! L12(SEQ ID NO: 293)  
GAT ATT GTG ATG ACC CAG ACT CCA CTC TCC CTG CCC  
GTC ACC CCT GGA GAG CCG GCC TCC ATC TCC TGC ! O11(SEQ ID NO: 294)  
GAT ATT GTG ATG ACC CAG ACT CCA CTC TCC CTG CCC  
GTC ACC CCT GGA GAG CCG GCC TCC ATC TCC TGC ! O1(SEQ ID NO: 295)  
GAT GTT GTG ATG ACT CAG TCT CCA CTC TCC CTG CCC  
GTC ACC CTT GGA CAG CCG GCC TCC ATC TCC TGC ! A17(SEQ ID NO: 296)  
GAT GTT GTG ATG ACT CAG TCT CCA CTC TCC CTG CCC  
GTC ACC CTT GGA CAG CCG GCC TCC ATC TCC TGC ! A1(SEQ ID NO: 297)  
GAT ATT GTG ATG ACC CAG ACT CCA CTC TCT CTG TCC  
GTC ACC CCT GGA CAG CCG GCC TCC ATC TCC TGC ! A18(SEQ ID NO: 298)  
GAT ATT GTG ATG ACC CAG ACT CCA CTC TCT CTG TCC  
GTC ACC CCT GGA CAG CCG GCC TCC ATC TCC TGC ! A2(SEQ ID NO: 299)  
GAT ATT GTG ATG ACT CAG TCT CCA CTC TCC CTG CCC  
GTC ACC CCT GGA GAG CCG GCC TCC ATC TCC TGC ! A19(SEQ ID NO: 300)  
GAT ATT GTG ATG ACT CAG TCT CCA CTC TCC CTG CCC  
GTC ACC CCT GGA GAG CCG GCC TCC ATC TCC TGC ! A3(SEQ ID NO: 301)  
GAT ATT GTG ATG ACC CAG ACT CCA CTC TCC TCA CCT  
GTC ACC CTT GGA CAG CCG GCC TCC ATC TCC TGC ! A23(SEQ ID NO: 302)

GAA ATT GTG TTG ACG CAG TCT CCA GGC ACC CTG TCT  
 TTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC ! A27 (SEQ ID NO: 303)  
 GAA ATT GTG TTG ACG CAG TCT CCA GCC ACC CTG TCT  
 TTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC ! A11 (SEQ ID NO: 304)  
 GAA ATA GTG ATG ACG CAG TCT CCA GCC ACC CTG TCT  
 GTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC ! L2 (SEQ ID NO: 305)  
 GAA ATA GTG ATG ACG CAG TCT CCA GCC ACC CTG TCT  
 GTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC ! L16 (SEQ ID NO: 306)  
 GAA ATT GTG TTG ACA CAG TCT CCA GCC ACC CTG TCT  
 TTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC ! L6 (SEQ ID NO: 307)  
 GAA ATT GTG TTG ACA CAG TCT CCA GCC ACC CTG TCT  
 TTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC ! L20 (SEQ ID NO: 308)  
 GAA ATT GTA ATG ACA CAG TCT CCA GCC ACC CTG TCT  
 TTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC ! L25 (SEQ ID NO: 309)  
 GAC ATC GTG ATG ACC CAG TCT CCA GAC TCC CTG GCT  
 GTG TCT CTG GGC GAG AGG GCC ACC ATC AAC TGC ! B3 (SEQ ID NO: 310)  
 GAA ACG ACA CTC ACG CAG TCT CCA GCA TTC ATG TCA  
 GCG ACT CCA GGA GAC AAA GTC AAC ATC TCC TGC ! B2 (SEQ ID NO: 311)  
 GAA ATT GTG CTG ACT CAG TCT CCA GAC TTT CAG TCT  
 GTG ACT CCA AAG GAG AAA GTC ACC ATC ACC TGC ! A26 (SEQ ID NO: 312)  
 GAA ATT GTG CTG ACT CAG TCT CCA GAC TTT CAG TCT  
 GTG ACT CCA AAG GAG AAA GTC ACC ATC ACC TGC ! A10 (SEQ ID NO: 313)  
 GAT GTT GTG ATG ACA CAG TCT CCA GCT TTC CTC TCT  
 GTG ACT CCA GGG GAG AAA GTC ACC ATC ACC TGC ! A14 (SEQ ID NO: 314)

Please delete Table 10 and replace it with the following table:

Table 10 Lambda FR1 GLG sequences

! VL1

CAG TCT GTG CTG ACT CAG CCA CCC TCG GTG TCT GAA  
 GCC CCC AGG CAG AGG GTC ACC ATC TCC TGT ! 1a  
(SEQ ID NO: 315)  
 cag tct gtg ctg acG cag ccG ccc tcA gtg tct gGG  
 gcc ccA Ggg cag agg gtc acc atc tcc tgC ! 1e

(SEQ ID NO: 316)

cag tct gtg ctg act cag cca ccc tcA gCg tct gGG  
Acc ccc Ggg cag agg gtc acc atc tcT tgt ! 1c

(SEQ ID NO: 317)

cag tct gtg ctg act cag cca ccc tcA gCg tct gGG  
Acc ccc Ggg cag agg gtc acc atc tcT tgt ! 1g

(SEQ ID NO: 318)

cag tct gtg Ttg acG cag ccG ccc tcA gtg tct gCG  
gcc ccA GgA cag aAg gtc acc atc tcc tgc ! 1b

! VL2

(SEQ ID NO: 319)

CAG TCT GCC CTG ACT CAG CCT CCC TCC GCG TCC GGG  
TCT CCT GGA CAG TCA GTC ACC ATC TCC TGC ! 2c

(SEQ ID NO: 320)

cag tct gcc ctg act cag cct cGc tcA gTg tcc ggg  
tct cct gga cag tca gtc acc atc tcc tgc! 2e

(SEQ ID NO: 321)

cag tct gcc ctg act cag cct Gcc tcc gTg tcT ggg  
tct cct gga cag tcG Atc acc atc tcc tgc ! 2a2

(SEQ ID NO: 322)

cag tct gcc ctg act cag cct ccc tcc gTg tcc ggg  
tct cct gga cag tca gtc acc atc tcc tgc ! 2d

(SEQ ID NO: 323)

cag tct gcc ctg act cag cct Gcc tcc gTg tcT ggg  
tct cct gga cag tcG Atc acc atc tcc tgc ! 2b2

! VL3

(SEQ ID NO: 324)

TCC TAT GAG CTG ACT CAG CCA CCC TCA GTG TCC GTG  
TCC CCA GGA CAG ACA GCC AGC ATC ACC TGC! 3r

(SEQ ID NO: 325)

tcc tat gag ctg act cag cca cTc tca gtg tcA gtg  
Gcc cTG gga cag acG gcc agG atT acc tgT ! 3j

(SEQ ID NO: 326)

tcc tat gag ctg acA cag cca ccc tcG gtg tcA gtg  
tcc cca gga caA acG gcc agG atc acc tgc! 3p

(SEQ ID NO: 327)

tcc tat gag ctg acA cag cca ccc tcG gtg tcA gtg  
tcc cTa gga cag aTG gcc agG atc acc tgc ! 3a

(SEQ ID NO: 328)

tCt tCt gag ctg act cag GAC cCt GcT gtg tCt gtg  
Gcc TTG gga cag aca gTc agG atc acA tgc ! 3l

(SEQ ID NO: 329)

tcc tat gTg ctg act cag cca ccc tca gtg tcA gtg  
Gcc cca gga Aag acG gcc agG atT acc tgT ! 3h

(SEQ ID NO: 330)

tcc tat gag ctg acA cag cTa ccc tcG gtg tcA gtg  
tcc cca gga cag aca gcc agG atc acc tgc ! 3e

(SEQ ID NO: 331)

tcc tat gag ctg aTG cag cca ccc tcG gtg tcA gtg  
tcc cca gga cag acG gcc agG atc acc tgc ! 3m

(SEQ ID NO: 332)

tcc tat gag ctg acA cag cca Tcc tca gtg tcA gtg  
tCt ccG gga cag aca gcc agG atc acc tgc ! V2-19

! VL4

(SEQ ID NO: 333)

CTG CCT GTG CTG ACT CAG CCC CCG TCT GCA TCT GCC  
TTG CTG GGA GCC TCG ATC AAG CTC ACC TGC ! 4c

(SEQ ID NO: 334)

cAg cct gtg ctg act caA TcA TcC tct gcC tct gcT  
tCC ctg gga Tcc tcg Gtc aag ctc acc tgc ! 4a

(SEQ ID NO: 335)

cAg cTt gtg ctg act caA TcG ccC tct gcC tct gcc  
tCC ctg gga gcc tcg Gtc aag ctc acc tgc ! 4b

! VL5

(SEQ ID NO: 336)

CAG CCT GTG CTG ACT CAG CCA CCT TCC TCC TCC GCA  
TCT CCT GGA GAA TCC GCC AGA CTC ACC TGC ! 5e

(SEQ ID NO: 337)

cag Gct gtg ctg act cag ccG Gct tcc CTc tCt gca  
tct cct gga gCa tcA gcc agT ctc acc tgc ! 5c

(SEQ ID NO: 338)

cag cct gtg ctg act cag cca Tct tcc CAT tCt gca  
tct Tct gga gCa tcA gTc aga ctc acc tgc ! 5b

! VL6

(SEQ ID NO: 339)

AAT TTT ATG CTG ACT CAG CCC CAC TCT GTG TCG GAG  
TCT CCG GGG AAG ACG GTA ACC ATC TCC TGC ! 6a

! VL7        (SEQ ID NO: 340)  
 CAG ACT GTG GTG ACT CAG GAG CCC TCA CTG ACT GTG  
 TCC CCA GGA GGG ACA GTC ACT CTC ACC TGT ! 7a  
(SEQ ID NO: 341)  
 cag Gct gtg gtg act cag gag ccc tca ctg act gtg  
 tcc cca gga ggg aca gtc act ctc acc tgt ! 7b

! VL8        (SEQ ID NO: 342)  
 CAG ACT GTG GTG ACC CAG GAG CCA TCG TTC TCA GTG  
 TCC CCT GGA GGG ACA GTC ACA CTC ACT TGT ! 8a

! VL9        (SEQ ID NO: 343)  
 CAG CCT GTG CTG ACT CAG CCA CCT TCT GCA TCA GCC  
 TCC CTG GGA GCC TCG GTC ACA CTC ACC TGC ! 9a

! VL10       (SEQ ID NO: 344)  
 CAG GCA GGG CTG ACT CAG CCA CCC TCG GTG TCC AAG  
 GGC TTG AGA CAG ACC GCC ACA CTC ACC TGC ! 10a  
(SEQ ID NO: 345)

Please delete Table 11 and replace it with the following table:

Table 11 RERSs found in human lambda FR1 GLGs

! There are 31 lambda GLGs

MlyI NnnnnnGACTC (SEQ ID NO: 346) 25

1: 6	3: 6	4: 6	6: 6	7: 6	8: 6
9: 6	10: 6	11: 6	12: 6	15: 6	16: 6
20: 6	21: 6	22: 6	23: 6	23: 50	24: 6
25: 6	25: 50	26: 6	27: 6	28: 6	30: 6
31: 6					

There are 23 hits at base# 6

- "- GAGTCNNNNNn (SEQ ID NO: 347) 1

26: 34

MwoI GCNNNNNnngc (SEQ ID NO: 348) 20

1: 9 2: 9 3: 9 4: 9 11: 9 11: 56  
 12: 9 13: 9 14: 9 16: 9 17: 9 18: 9  
 19: 9 20: 9 23: 9 24: 9 25: 9 26: 9  
 30: 9 31: 9

There are 19 hits at base# 9

HinfI Gantc 27  
 1: 12 3: 12 4: 12 6: 12 7: 12 8: 12  
 9: 12 10: 12 11: 12 12: 12 15: 12 16: 12  
 20: 12 21: 12 22: 12 23: 12 23: 46 23: 56  
 24: 12 25: 12 25: 56 26: 12 26: 34 27: 12  
 28: 12 30: 12 31: 12

There are 23 hits at base# 12

PleI gactc 25  
 1: 12 3: 12 4: 12 6: 12 7: 12 8: 12  
 9: 12 10: 12 11: 12 12: 12 15: 12 16: 12  
 20: 12 21: 12 22: 12 23: 12 23: 56 24: 12  
 25: 12 25: 56 26: 12 27: 12 28: 12 30: 12  
 31: 12

There are 23 hits at base# 12

-"- gagtc 1  
 26: 34

DdeI Ctnag 32  
 1: 14 2: 24 3: 14 3: 24 4: 14 4: 24  
 5: 24 6: 14 7: 14 7: 24 8: 14 9: 14  
 10: 14 11: 14 11: 24 12: 14 12: 24 15: 5  
 15: 14 16: 14 16: 24 19: 24 20: 14 23: 14  
 24: 14 25: 14 26: 14 27: 14 28: 14 29: 30  
 30: 14 31: 14

There are 21 hits at base# 14

BsaJI Ccnngg 38  
 1: 23 1: 40 2: 39 2: 40 3: 39 3: 40  
 4: 39 4: 40 5: 39 11: 39 12: 38 12: 39  
 13: 23 13: 39 14: 23 14: 39 15: 38 16: 39

17: 23    17: 39    18: 23    18: 39    21: 38    21: 39  
 21: 47    22: 38    22: 39    22: 47    26: 40    27: 39  
 28: 39    29: 14    29: 39    30: 38    30: 39    30: 47  
 31: 23    31: 32

There are 17 hits at base# 39

There are 5 hits at base# 38

There are 5 hits at base# 40 Makes cleavage ragged.

MnlI cctc

35

1: 23    2: 23    3: 23    4: 23    5: 23    6: 19  
 6: 23    7: 19    8: 23    9: 19    9: 23    10: 23  
 11: 23    13: 23    14: 23    16: 23    17: 23    18: 23  
 19: 23    20: 47    21: 23    21: 29    21: 47    22: 23  
 22: 29    22: 35    22: 47    23: 26    23: 29    24: 27  
 27: 23    28: 23    30: 35    30: 47    31: 23

There are 21 hits at base# 23

There are 3 hits at base# 19

There are 3 hits at base# 29

There are 1 hits at base# 26

There are 1 hits at base# 27 These could make cleavage ragged.

-"- gagg

7

1: 48    2: 48    3: 48    4: 48    27: 44    28: 44  
 29: 44

BssKI Nccngg

39

1: 40    2: 39    3: 39    3: 40    4: 39    4: 40  
 5: 39    6: 31    6: 39    7: 31    7: 39    8: 39  
 9: 31    9: 39    10: 39    11: 39    12: 38    12: 52  
 13: 39    13: 52    14: 52    16: 39    16: 52    17: 39  
 17: 52    18: 39    18: 52    19: 39    19: 52    21: 38  
 22: 38    23: 39    24: 39    26: 39    27: 39    28: 39  
 29: 14    29: 39    30: 38

There are 21 hits at base# 39

There are 4 hits at base# 38

There are 3 hits at base# 31

There are 3 hits at base# 40 Ragged

BstNI CCwgg 30

1: 41	2: 40	5: 40	6: 40	7: 40	8: 40
9: 40	10: 40	11: 40	12: 39	12: 53	13: 40
13: 53	14: 53	16: 40	16: 53	17: 40	17: 53
18: 40	18: 53	19: 53	21: 39	22: 39	23: 40
24: 40	27: 40	28: 40	29: 15	29: 40	30: 39

There are 17 hits at base# 40

There are 7 hits at base# 53

There are 4 hits at base# 39

There are 1 hits at base# 41 Ragged

PspGI ccwgg 30

1: 41	2: 40	5: 40	6: 40	7: 40	8: 40
9: 40	10: 40	11: 40	12: 39	12: 53	13: 40
13: 53	14: 53	16: 40	16: 53	17: 40	17: 53
18: 40	18: 53	19: 53	21: 39	22: 39	23: 40
24: 40	27: 40	28: 40	29: 15	29: 40	30: 39

There are 17 hits at base# 40

There are 7 hits at base# 53

There are 4 hits at base# 39

There are 1 hits at base# 41

ScrFI CCngg 39

1: 41	2: 40	3: 40	3: 41	4: 40	4: 41
5: 40	6: 32	6: 40	7: 32	7: 40	8: 40
9: 32	9: 40	10: 40	11: 40	12: 39	12: 53
13: 40	13: 53	14: 53	16: 40	16: 53	17: 40
17: 53	18: 40	18: 53	19: 40	19: 53	21: 39
22: 39	23: 40	24: 40	26: 40	27: 40	28: 40
29: 15	29: 40	30: 39			

There are 21 hits at base# 40

There are 4 hits at base# 39

There are 3 hits at base# 41

MaeIII gtnac 16



1: 52      2: 52      3: 52      4: 52      5: 52      6: 52  
 7: 52      9: 52      26: 52      27: 10      27: 52      28: 10  
 28: 52      29: 10      29: 52      30: 52

There are 13 hits at base# 52

Tsp45I gtsac

15

1: 52      2: 52      3: 52      4: 52      5: 52      6: 52  
 7: 52      9: 52      27: 10      27: 52      28: 10      28: 52  
 29: 10      29: 52      30: 52

There are 12 hits at base# 52

HphI tcacc

26

1: 53      2: 53      3: 53      4: 53      5: 53      6: 53  
 7: 53      8: 53      9: 53      10: 53      11: 59      13: 59  
 14: 59      17: 59      18: 59      19: 59      20: 59      21: 59  
 22: 59      23: 59      24: 59      25: 59      27: 59      28: 59  
 30: 59      31: 59

There are 16 hits at base# 59

There are 10 hits at base# 53

BspMI ACCTGCNNNNn (SEQ ID NO: 349) 14

11: 61      13: 61      14: 61      17: 61      18: 61      19: 61  
 20: 61      21: 61      22: 61      23: 61      24: 61      25: 61  
 30: 61      31: 61

There are 14 hits at base# 61 Goes into CDR1

Please delete Table 13 and replace it with the following table:

Table 13

The following list of enzymes was taken from  
<http://rebase.neb.com/cgi-bin/asymmlist>.

I have removed the enzymes that a) cut within the recognition, b) cut on both sides of the recognition, or c) have fewer than 2 bases between recognition and closest cut site.

REBASE Enzymes

04/13/2001

Type II restriction enzymes with asymmetric recognition sequences:

Enzymes	Recognition Sequence	Isoschizomers	Suppliers
AarI	CACCTGCNNNN^NNNN_	-	Y
AceIII	CAGCTCNNNNNNNN^NNNN_	-	-
Bbr7I	GAAGACNNNNNNNN^NNNN_	-	-
BbvI	GCAGCNNNNNNNN^NNNN_	-	Y
BbvII	GAAGACNN^NNNN_	-	-
Bce83I	CTTGAGNNNNNNNNNNNNNNNN^	-	-
BceAI	ACGGCNNNNNNNNNNNNNN^NN_	-	Y
BceFI	ACGGCNNNNNNNNNNNNNN^N_	-	-
BciVI	GTATCCNNNNN_N^	BfuI	Y
BfiI	ACTGGGNNNN_N^	BmrI	Y
BinI	GGATCNNNN^N_	-	-
BscAI	GCATCNNNN^NN_	-	-
BseRI	GAGGAGNNNNNNNNNN^	-	Y
BsmFI	GGGACNNNNNNNNNNNN^NNNN_	BspLU11III	Y
BspMI	ACCTGCNNNN^NNNN_	Acc36I	Y
EciI	GGCGGANNNNNNNNNN^	-	Y
Eco57I	CTGAAGNNNNNNNNNNNNNNNN^	BspKT5I	Y
FauI	CCCGCNNNN^NN_	BstFZ438I	Y
FokI	GGATGNNNNNNNNNN^NNNN_	BstPZ418I	Y
GsuI	CTGGAGNNNNNNNNNNNNNNNN^	-	Y
HgaI	GACGCNNNNN^NNNNN_	-	Y
HphI	GGTGANNNNNNN_N^	AsuHPI	Y
MboII	GAAGANNNNNNN_N^	-	Y
MlyI	GAGTCNNNNN^	SchI	Y
MmeI	TCCRACNNNNNNNNNNNNNNNN^	-	-
MnlI	CCTCNNNNNN_N^	-	Y
PleI	GAGTCNNNN^N_	PpsI	Y
RleAI	CCCACANNNNNNNNNN^	-	-
SfaNI	GCATCNNNNN^NNNN_	BspST5I	Y
SspD5I	GGTGANNNNNNNN^	-	-
Sth132I	CCCGNNNN^NNNN_	-	-
StsI	GGATGNNNNNNNNNN^NNNN_	-	-
TaqII	GACCGANNNNNNNNNN^, CACCCANNNNNNNNNN^	-	-
Tth111II	CAARCANNNNNNNNNN^	-	-
UbaPI	CGAACG	-	-

(SEQ ID NOS 356-390, respectively in order of appearance)

The notation is ^ means cut the upper strand and \_ means cut the lower strand. If the upper and lower strand are cut at the same place, then only ^ appears.

Please delete Table 14 and replace it with the following table:

Table 14	5'- <u>cAcATccgTg</u> TTgTT <u>cAcggATgTg</u> -3' (SEQ ID NO: 350)
(FOKIact)	
(VHEx881)	5'-AATAGTAGAc TgcAgTgTcc TcAgccctTA AgcTgTtCAT cTgcAAGTAG- AgAgTATTctT TAGAgTTgTc TctAgAcTTA gTgAAgcg-3' (SEQ ID NO: 351)
!	! note that VHEx881 is the reverse complement of the ON below
!	! [RC] 5'-cgCttcacTaag-
!	! Scab.....
!	! Synthetic 3-23 as in Table 206
!	! TCT AGA gac aac tct aag aat act ctc tac ttg cag atg -
!	! XbaI...
!	! aac agC TTA AGg gct gag gac aCT GCA Gtc tat t-3' (SEQ ID NO: 352)
!	! AflII...
(VHBA881)	5'-cgCttcacTaag- TCT AGA gac aac tct aag aat act ctc tac ttg cag atg -
(VHBB881)	aac agC TTA AGg gct gag gac aCT GCA Gtc tat tgt gcg ag-3' (SEQ ID NO: 353)
	5'-cgCttcacTaag- TCT AGA gac aac tct aag aat act ctc tac ttg cag atg -
(VH881PCR)	aac agC TTA AGg gct gag gac aCT GCA Gtc tat tgt Acg ag-3' (SEQ ID NO: 354)
	5'-cgCttcacTaag TCT AGA gac aac -3' (SEQ ID NO: 355)



Case II

Stem 10, loop 5, stem 10, recognition 18

(SEQ ID NO: 3)

5' - ...gtgtatt|agac-tgctgcc..Substrate....-3'

┌T┐  
T gtgCCTACac  
└┐  
C cacGGATGtg-3' (SEQ ID NO: 4)  
└TT┘

Case III (Case I rotated 180 degrees)

Stem 11, loop 5, stem 11, recognition 20

┌T┐  
T TgtgCCTACac-5' (SEQ ID NO: 5)  
G AcacGGATGtg┐  
└TT┘  
gtgtctt|acag-tccattctg-3' Adapter  
3' - ...cacagaa-tgtc|aggtaagac..substrate....-5'  
(SEQ ID NO: 6)

Case IV (Case II rotated 180 degrees)

Stem 11, loop 4, stem 11, recognition 17

(SEQ ID NO: 7)

3' - gtGTAGGcacc T  
┌T┐  
└┐  
5' - atcgag|tctc-actgagc  
└T┘  
Substrate 3' - ...tagctc-agag|tgactcg...-5' (SEQ ID NO: 8)

BseRI

(SEQ ID NO: 9) | sites of cleavage

5' - cacGAGGAGnnnnnnnnnn|nnnnn-3'  
3' - gtgctcctcnnnnnnnnn|nnnnnnn-5'  
RECOG  
NITion of BseRI

Stem 11, loop 5, stem 11, recognition 19

3' - .....gaacat|cg-ttaagccagta.....5' (SEQ ID NO: 10)

┌T-T┐  
C GCTGAGGAGTC-┐  
└┐  
T cgactcctcag-5' An adapter for BseRI to cleave the substrate  
above.  
└T┘ (SEQ ID NO: 11)

Please delete Table 16 and replace it with the following table:

Table 16 Human heavy chains bases 88.1 to 94.2

Number of sequences..... 840

Id	Ntot	Number of Mismatches.....							Name	Probe Sequence.....	Dot form.....
		0	1	2	3	4	5	6			
1	364	152	97	76	26	7	4	2	0	VHS881-1.1 gctgtgtattactgtgcgag	gctgtgtattactgtgcgag
2	265	150	60	33	13	5	4	0	0	VHS881-1.2 gccgtgtattactgtgcgag	.c.....
3	96	14	34	16	10	5	7	9	1	VHS881-2.1 gccgtatattactgtgcgag	.c.a.....
4	20	0	3	4	9	2	2	0	0	VHS881-4.1 gccgtgtattactgtgcgag	.c.....a....
5	95	25	36	18	11	2	2	0	1	VHS881-9.1 gccatgtattactgtgcgag	.ca.....
840	341	230	147	69	21	19	11	2	2	<b>(SEQ ID NOS 391-395, respectively in order of appearance)</b>	
341	571	718	787	808	827	838	840				

88 89 90 91 92 93 94 95 Codon number as in Table 195

Recognition..... Stem..... Loop..... Stem.....  
 (VHS881-1.1) 5'-gctgtgtat|tact-gtgcgag cAcATccgTg TTgTT cAcgATcTg-3'  
 (VHS881-1.2) 5'-gccgtgtat|tact-gtgcgag cAcATccgTg TTgTT cAcgATcTg-3'  
 (VHS881-2.1) 5'-gccgtat|tact-gtgcgag cAcATccgTg TTgTT cAcgATcTg-3'  
 (VHS881-4.1) 5'-gccgtgtat|tact-gtgcgag cAcATccgTg TTgTT cAcgATcTg-3'  
 (VHS881-9.1) 5'-gccatgtat|tact-gtgcgag cAcATccgTg TTgTT cAcgATcTg-3'  
 | site of substrate cleavage

**(Sequences in the left column above are SEQ ID NOS 391-395, respectively in order of appearance; sequences in the right column are all SEQ ID NO: 396)**

(FOK1act) 5'-cAcATccgTg TTgTT cAcgATcTg-3' (SEQ ID NO: 396)

(VHEx881) 5'-AATAgTAgAc TgcAgTgTcc TcAgcccTTA AgcTgTTcAT cTgcAAgTAg-  
 AgAgTATTcT TAgAgTTgTc TcTAgAcTTA gTgAAgcg-3' (SEQ ID NO: 397)

! note that VHEx881 is the reverse complement of the ON below

! [RC] 5'-cgCttcacTaa-

! Scab.....

! Synthetic 3-23 as in Table 206

! |TCT|AGA|gac|aac|tct|aat|act|ctc|tac|ttg|cag|atg|-

```

! XbaI...
! |aac|agC|TTA|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat|t-3'
! AflI...
(VHBA881) 5'-cgCttcacTaa-
|TCT|AGA|gac|aac|tct|aag|aat|act|ctc|tac|ttg|cag|atg|-
|aac|agC|TTA|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tgt|gcg|ag-3' (SEQ ID NO: 398)
(VHBB881) 5'-cgCttcacTaa-
|TCT|AGA|gac|aac|tct|aag|aat|act|ctc|tac|ttg|cag|atg|-
|aac|agC|TTA|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tgt|Acg|ag-3' (SEQ ID NO: 618)
(VH881PCR) 5'-cgCttcacTaa|TCT|AGA|gac|aac-3' (SEQ ID NO: 399)

```

Please delete Table 17 and replace it with the following table:

Table 17: Kappa, bases 12-30

! ID	Ntot	0	1	2	3	4	5	6	Name	Sequence.....	Dot Form.....
! 1	84	40	21	20	1	2	0	0	SK12O12	gaccagttcttcactctcc	gaccagttcttcactctcc (residues 26-44 of SEQ ID NO: 400)
! 2	32	19	3	6	2	1	0	1	SK12A17	gactcagttcttcactctcc	...t.....ct.... (residues 26-44 of SEQ ID NO: 401)
! 3	26	17	8	1	0	0	0	0	SK12A27	gacgcagttcttcaggcacc	...g.....gg.a.. (residues 26-44 of SEQ ID NO: 402)
! 4	40	21	18	1	0	0	0	0	SK12A11	gacgcagttcttcaggcacc	...g.....g.a.. (residues 26-44 of SEQ ID NO: 403)
! 182	97	50	28	3	3	0	1				
! 97	147	175	178	181	181	182					

URE adapters:

```

! Stem..... Loop. Stem..... Recognition.....
(SzKB1230-O12) 5'-cAcATccgTg TTgTT cAcggATgTg ggAggATggAgAcTgggTc-3' (SEQ ID NO: 400)
! [RC] 5'-gaccagttcttcactctcc cAcATccgTg AACAA cAcggATgTg-3'
! Recognition..... Stem..... loop. Stem.....
! FokI. FokI.
!

```

```

! Stem..... Loop. Stem..... Recognition.....

```

(SzKB1230-A17) 5'-cAcATccgTg TTgTT cAcggATgTg ggAgAgTggAgAcTgAgTc-3' (SEQ ID NO: 401)

! [RC] 5'-gacTcagtctcactctcc cAcATccgTg AACAA cAcggATgTg-3'

! Recognition..... Stem..... loop. Stem.....

! FokI. FokI.

! Stem..... Loop. Stem..... Recognition.....

(SzKB1230-A27) 5'-cAcATccgTg TTgTT cAcggATgTg ggTgccTggAgAcTggTc-3' (SEQ ID NO: 402)

! [RC] 5'-gacgcagtctccaggcacc cAcATccgTg AACAA cAcggATgTg-3'

! Recognition..... Stem..... loop. Stem.....

! FokI. FokI.

! Stem..... Loop. Stem..... Recognition.....

(SzKB1230-A11) 5'-cAcATccgTg TTgTT cAcggATgTg ggTggcTggAgAcTggTc-3' (SEQ ID NO: 403)

! [RC] 5'-gacgcagtctccaggcacc cAcATccgTg AACAA cAcggATgTg-3'

! Recognition..... Stem..... loop. Stem.....

! FokI. FokI.

What happens in the upper strand:

(SzKB1230-O12\*) 5'-gac cca gtc | tcc a-tc ctc c-3' (residues 26-44 of SEQ ID NO: 400)

! | Site of cleavage in substrate

(SzKB1230-A17\*) 5'-gac tca gtc | tcc a-ct ctc c-3' (residues 26-44 of SEQ ID NO: 401)

!

(SzKB1230-A27\*) 5'-gac gca gtc | tcc a-gg cac c-3' (residues 26-44 of SEQ ID NO: 402)

!

(SzKB1230-A11\*) 5'-gac gca gtc | tcc a-gc cac c-3' (residues 26-44 of SEQ ID NO: 403)

(kapeXtURE) 5'-ccTctactctTgTcAcAgTgcAcAA gAc ATc cAg-3' !sense strand (SEQ ID NO: 404)  
Scab.....ApaLI.

(kapeXtUREPCR) 5'-ccTctactctTgTcAcAgTg-3' (SEQ ID NO: 405)  
Scab.....



(kaBR01UR) 5' -ggAggATggA cTggATgTcTtTgTgcAcTgTgAcAAGAgTA gAgg-3' (SEQ ID NO: 406)  
 ! [RC] 5' -ccTctactctTgTcAcAgTgcAcAA gAc ATc cAG tcc a-tc ctc c-3' ON above is R.C. of this one  
 (kaBR02UR) 5' -ggAgAgTggA cTggATgTcTtTgTgcAcTgTgAcAAGAgTA gAgg-3' (SEQ ID NO: 407)  
 ! [RC] 5' -ccTctactctTgTcAcAgTgcAcAA gAc ATc cAG tcc a-tc ctc c-3' ON above is R.C. of this one  
 (kaBR03UR) 5' -ggTgcTggA cTggATgTcTtTgTgcAcTgTgAcAAGAgTA gAgg-3' (SEQ ID NO: 408)  
 ! [RC] 5' -ccTctactctTgTcAcAgTgcAcAA gAc ATc cAG tcc a-gg cac c-3' ON above is R.C. of this one  
 (kaBR04UR) 5' -ggTggcTggA cTggATgTcTtTgTgcAcTgTgAcAAGAgTA gAgg-3' (SEQ ID NO: 409)  
 ! [RC] 5' -ccTctactctTgTcAcAgTgcAcAA gAc ATc cAG tcc a-gc cac c-3' ON above is R.C. of this one  
 Scab.....ApaLI.

Please delete Table 18 and replace it with the following table:

Table 18 Lambda URE adapters bases 13.3 to 19.3

[illegible]

(VL133-3l) 5'-cAcATccgTg TTgTT cAcggATgTg gAcTgTcTgTcccAAggcc-3' (SEQ ID NO: 411)  
 ! [RC] 5'-ggcctgggacagcagtc cAcATccgTg AAcAA cAcggATgTg-3'  
 ! Recognition..... Stem..... Loop. Stem.....  
 !  
 ! Stem..... loop. Stem..... Recognition.....  
 (VL133-2c) 5'-cAcATccgTg TTgTT cAcggATgTg gAcTgAcTgTccAggAgAc-3' (SEQ ID NO: 412)  
 ! [RC] 5'-gtctctgggacagtc cAcATccgTg AAcAA cAcggATgTg-3'  
 ! Recognition..... Stem..... Loop. Stem.....  
 !  
 ! Stem..... loop. Stem..... Recognition.....  
 (VL133-1c) 5'-cAcATccgTg TTgTT cAcggATgTg gAcctTcTgcccTggggcc-3' (SEQ ID NO: 413)  
 ! [RC] 5'-ggccccaggcagagggtc cAcATccgTg AAcAA cAcggATgTg-3'

What happens in the top strand:

! | site of cleavage in the upper strand  
 (VL133-2a2\*) 5'-g tct cct g | ga cag tcg atc (residues 632-635 of SEQ ID NO: 410)  
 !  
 (VL133-3l\*) 5'-g gcc ttg g | ga cag aca gtc (residues 632-635 of SEQ ID NO: 411)  
 !  
 (VL133-2c\*) 5'-g tct cct g | ga cag tca gtc (residues 632-635 of SEQ ID NO: 412)  
 !  
 (VL133-1c\*) 5'-g gcc cca g | gg cag agg gtc (residues 632-635 of SEQ ID NO: 413)  
 !  
 ! The following Extenders and Bridges all encode the AA sequence of 2a2 for codons 1-15  
 ! 1  
 (ON\_LamEx133) 5'-ccTcTgAcTgAgT gca cAg -  
 !  
 ! 2 3 4 5 6 7 8 9 10 11 12  
 AGt gcT TtA acC caA ccG gcT AGT gtT AGC ggT-  
 !  
 ! 13 14 15  
 tcC ccG g ! 2a2 (SEQ ID NO: 414)  
 ! 1

(ON\_LamB1-133) [RC] 5'-ccTcTgAcTgAgT gca cAg -

2 3 4 5 6 7 8 9 10 11 12

AGt gcT TtA acC caA ccG gcT AGT gtT AGC ggT-

13 14 15

tcC ccG g ga cag tgc at-3'! (SEQ ID NO: 415) 2a2 N.B. the actual seq is the

reverse complement of the

one shown.

(ON\_LamB2-133) [RC] 5'-ccTcTgAcTgAgT gca cAg -

2 3 4 5 6 7 8 9 10 11 12

AGt gcT TtA acC caA ccG gcT AGT gtT AGC ggT-

13 14 15

tcC ccG g ga cag aca gt-3'! 3! (SEQ ID NO: 416) N.B. the actual seq is the

reverse complement of the

one shown.

(ON\_LamB3-133) [RC] 5'-ccTcTgAcTgAgT gca cAg -

2 3 4 5 6 7 8 9 10 11 12

AGt gcT TtA acC caA ccG gcT AGT gtT AGC ggT-

13 14 15

tcC ccG g ga cag tca gt-3'! 2c (SEQ ID NO: 417) N.B. the actual seq is the

reverse complement of the

one shown.

(ON\_LamB4-133) [RC] 5'-ccTcTgAcTgAgT gca cAg -

1 :  
2 3 4 5 6 7 8 9 10 11 12  
AGT gcT TtA acC caA ccG gcT AGT gtT AGC ggT-s

13 14 15

!                    tcC ccG g gg cag agg gt-3' ! 1c (SEQ ID NO: 418) N.B. the actual seq is the  
!                    reverse complement of the  
!                    one shown.

(ON\_Lam133PCR) 5'-ccTcTgAcTgAgT gcA cAg AGt gc-3' (SEQ ID NO: 419)

Please delete Table 19 and replace it with the following table:

Table 19: Cleavage of 75 human light chains.

Enzyme	Recognition*	Nch	Ns	Planned location of site
AfeI	AGCgct	0	0	
AflII	Cttaag	0	0	HC FR3
AgeI	Accggt	0	0	
AscI	GGcgcgcc	0	0	After LC
BglII	Agatct	0	0	
BsiWI	Cgtacg	0	0	
BspDI	ATcgat	0	0	
BssHII	Gcgcg	0	0	
BstBI	TTcgaa	0	0	
DraIII	CACNNNgtg	0	0	
EagI	Cggccg	0	0	
FseI	GGCCGGcc	0	0	
FspI	TGCgca	0	0	
HpaI	GTTaac	0	0	
MfeI	Caattg	0	0	HC FR1
MluI	Acgctg	0	0	
NcoI	Ccatgg	0	0	Heavy chain signal
NheI	Gctagc	0	0	HC/anchor linker
NotI	GCggccgc	0	0	In linker after HC
NruI	TCGcga	0	0	
PacI	TTAATtaa	0	0	
PmeI	GTTTaaac	0	0	
PmlI	CACgtg	0	0	
PvuI	CGATcg	0	0	
SacII	CCGCgg	0	0	
SalI	Gtcgac	0	0	
SfiI	GGCCNNNNnggcc	0	0	Heavy Chain signal (SEQ ID NO: 436)
SgfI	GCGATcgc	0	0	
SnaBI	TACgta	0	0	
StuI	AGGcct	0	0	
XbaI	Tctaga	0	0	HC FR3
AatII	GACGTc	1	1	
AclI	AAcggt	1	1	
AseI	ATtaat	1	1	
BsmI	GAATGCN	1	1	
BspEI	Tccgga	1	1	HC FR1 (SEQ ID NO: 437)
BstXI	CCANNNNNntgg	1	1	HC FR2 (SEQ ID NO: 438)
DrdI	GACNNNNnngtc	1	1	
HindIII	Aagctt	1	1	
PciI	Acatgt	1	1	
SapI	gaagagc	1	1	
ScaI	AGTact	1	1	
SexAI	Accwgt	1	1	
SpeI	Actagt	1	1	
TliI	Ctcgag	1	1	
XhoI	Ctcgag	1	1	
BcgI	cgannnnntgc	2	2	(SEQ ID NO: 439)
BlpI	GCTnagc	2	2	
BssSI	Ctcgtg	2	2	
BstAPI	GCANNNNntgc	2	2	(SEQ ID NO: 440)
EspI	GCTnagc	2	2	
KasI	Ggcgcc	2	2	
PflMI	CCANNNNntgg	2	2	(SEQ ID NO: 441)

XmnI	GAANNnnttc	2	2	<u>(SEQ ID NO: 442)</u>
<b>ApaLI</b>	<b>Gtgcac</b>	<b>3</b>	<b>3</b>	<b>LC signal seq</b>
NaeI	GCCggc	3	3	
NgoMI	Gccggc	3	3	
PvuII	CAGctg	3	3	
RsrII	CGgwccg	3	3	
BsrBI	GAGcgg	4	4	
BsrDI	GCAATGNNn	4	4	
BstZ17I	GTAtac	4	4	
EcoRI	Gaattc	4	4	
SphI	GCATGc	4	4	
SspI	AATatt	4	4	
AccI	GTmkac	5	5	
BclI	Tgatca	5	5	
BsmBI	Nnnnnngagacg	5	5	<u>(SEQ ID NO: 443)</u>
BsrGI	Tgtaca	5	5	
DraI	TTTaaa	6	6	
<b>NdeI</b>	<b>CAtatg</b>	<b>6</b>	<b>6</b>	<b>HC FR4</b>
SwaI	ATTTaaat	6	6	
BamHI	Ggatcc	7	7	
SacI	GAGCTc	7	7	
BciVI	GTATCCNNNNNN	8	8	<u>(SEQ ID NO: 444)</u>
BsaBI	GATNNnnatc	8	8	<u>(SEQ ID NO: 619)</u>
NsiI	ATGCAt	8	8	
<b>Bsp120I</b>	<b>Gggccc</b>	<b>9</b>	<b>9</b>	<b>CH1</b>
<b>ApaI</b>	<b>GGGCCc</b>	<b>9</b>	<b>9</b>	<b>CH1</b>
PspOoMI	Gggccc	9	9	
BspHI	Tcatga	9	11	
EcoRV	GATatc	9	9	
AhdI	GACNNNnngtc	11	11	<u>(SEQ ID NO: 445)</u>
BbsI	GAAGAC	11	14	
PsiI	TTataa	12	12	
BsaI	GGTCTCnnnnn	13	15	<u>(SEQ ID NO: 446)</u>
XmaI	Cccggg	13	14	
AvaI	Cycgrg	14	16	
BglI	GCCNNNNnggc	14	17	<u>(SEQ ID NO: 447)</u>
AlwNI	CAGNNNctg	16	16	
BspMI	ACCTGC	17	19	
XcmI	CCANNNNNnnnntgg	17	26	<u>(SEQ ID NO: 448)</u>
<b>BstEII</b>	<b>Ggtnacc</b>	<b>19</b>	<b>22</b>	<b>HC FR4</b>
Sse8387I	CCTGCagg	20	20	
AvrII	Cctagg	22	22	
HincII	GTYrac	22	22	
BsgI	GTGCAG	27	29	
MscI	TGGcca	30	34	
BseRI	NNnnnnnnnnctcctc	32	35	<u>(SEQ ID NO: 449)</u>
Bsu36I	CCtnagg	35	37	
PstI	CTGCAG	35	40	
EciI	nnnnnnnnntccgcc	38	40	<u>(SEQ ID NO: 450)</u>
PpuMI	RGgwccy	41	50	
StyI	Ccwwgg	44	73	
EcoO109I	RGgnccy	46	70	
Acc65I	Ggtacc	50	51	
KpnI	GGTACc	50	51	
BpmI	ctccag	53	82	
AvaII	Ggwcc	71	124	

\* cleavage occurs in the top strand after the last upper-case base.  
For REs that cut palindromic sequences, the lower strand is cut at the symmetrical site.

Please delete Table 20 and replace it with the following table:

Table 20: Cleavage of 79 human heavy chains

Enzyme	Recognition	Nch	Ns	Planned location of site
AfeI	AGCgct	0	0	
AflII	Cttaag	0	0	HC FR3
AscI	GGcgcgcc	0	0	After LC
BsiWI	Cgtacg	0	0	
BspDI	ATcgat	0	0	
BssHII	Gcgcg	0	0	
FseI	GGCCGGcc	0	0	
HpaI	GTTaac	0	0	
NheI	Gctagc	0	0	HC Linker
NotI	GCggcgc	0	0	In linker, HC/anchor
NruI	TCGcga	0	0	
NsiI	ATGCA	0	0	
PacI	TTAATtaa	0	0	
PciI	Acatgt	0	0	
PmeI	GTTTaaac	0	0	
PvuI	CGATcg	0	0	
RsrII	CGgwccg	0	0	
SapI	gaagagc	0	0	
SfiI	GGCCNNNNnggcc	0	0	HC signal seq (SEQ ID NO: 420)
SgfI	GCGATcg	0	0	
SwaI	ATTTaaat	0	0	
AclI	AAcggt	1	1	
AgeI	Accggt	1	1	
AseI	ATta	1	1	
AvrII	Cctagg	1	1	
BsmI	GAATGCN	1	1	
BsrBI	GAGcgg	1	1	
BsrDI	GCAATGNNn	1	1	
DraI	TTTaaa	1	1	
FspI	TGCgca	1	1	
HindIII	Aagctt	1	1	
MfeI	Caattg	1	1	HC FR1
NaeI	GCCggc	1	1	
NgoMI	Gccggc	1	1	
SpeI	Actagt	1	1	
Acc65I	Ggtacc	2	2	
BstBI	TTcgaa	2	2	
KpnI	GGTACc	2	2	
MluI	Acgcgt	2	2	
NcoI	Ccatgg	2	2	In HC signal seq
NdeI	CAtatg	2	2	HC FR4
PmlI	CACgtg	2	2	
XcmI	CCANNNNNnnnntgg	2	2	(SEQ ID NO: 421)
BcgI	cgannnnnntgc	3	3	(SEQ ID NO: 422)
BclI	Tgatca	3	3	

BglI	GCCNNNNnggc	3	3	<u>(SEQ ID NO: 423)</u>
BsaBI	GATNNnnatc	3	3	<u>(SEQ ID NO: 424)</u>
BsrGI	Tgtaca	3	3	
SnaBI	TACgta	3	3	
Sse8387I	CCTGCAGg	3	3	
<b>ApaLI</b>	<b>Gtgcac</b>	<b>4</b>	<b>4</b>	LC Signal/FR1
BspHI	Tcatga	4	4	
BssSI	Ctcgtg	4	4	
PsiI	TTataa	4	5	
SphI	GCATGc	4	4	
AhdI	GACNNNNngtc	5	5	<u>(SEQ ID NO: 425)</u>
<b>BspEI</b>	<b>Tccgga</b>	<b>5</b>	<b>5</b>	HC FR1
MscI	TGGcca	5	5	
SacI	GAGCTc	5	5	
ScaI	AGTact	5	5	
SexAI	Accwggg	5	6	
SspI	AATatt	5	5	
TliI	Ctcgag	5	5	
XhoI	Ctcgag	5	5	
BbsI	GAAGAC	7	8	
BstAPI	GCANNNNntgc	7	8	<u>(SEQ ID NO: 426)</u>
BstZ17I	GTAtac	7	7	
EcoRV	GATatc	7	7	
EcoRI	Gaattc	8	8	
BlpI	GCtnagc	9	9	
Bsu36I	CCtnagg	9	9	
DraIII	CACNNNgtg	9	9	
EspI	GCtnagc	9	9	
StuI	AGGcct	9	13	
<b>XbaI</b>	<b>Tctaga</b>	<b>9</b>	<b>9</b>	HC FR3
<b>Bsp120I</b>	<b>Gggccc</b>	<b>10</b>	<b>11</b>	CH1
<b>ApaI</b>	<b>GGGCCc</b>	<b>10</b>	<b>11</b>	CH1
PspOoMI	Gggccc	10	11	
BciVI	GTATCCNNNNNN	11	11	<u>(SEQ ID NO: 427)</u>
SalI	Gtcgac	11	12	
DrdI	GACNNNNnngtc	12	12	<u>(SEQ ID NO: 428)</u>
KasI	Ggcgcc	12	12	
XmaI	Cccggg	12	14	
BglII	Agatct	14	14	
HincII	GTYrac	16	18	
BamHI	Ggatcc	17	17	
PflMI	CCANNNNntgg	17	18	<u>(SEQ ID NO: 429)</u>
BsmBI	Nnnnnngagacg	18	21	<u>(SEQ ID NO: 430)</u>
<b>BstXI</b>	<b>CCANNNNNntgg</b>	<b>18</b>	<b>19</b>	HC FR2 <u>(SEQ ID NO: 431)</u>
XmnI	GAANNnttc	18	18	<u>(SEQ ID NO: 432)</u>
SacII	CCGCgg	19	19	
PstI	CTGCAg	20	24	
PvuII	CAGctg	20	22	
AvaI	Cycgrg	21	24	
EagI	Cggccg	21	22	
AatII	GACGTc	22	22	
BspMI	ACCTGC	27	33	
AccI	GTmkac	30	43	
StyI	Ccwwgg	36	49	
AlwNI	CAGNNNctg	38	44	
BsaI	GGTCTCnnnn	38	44	<u>(SEQ ID NO: 433)</u>
PpuMI	RGgwccy	43	46	



BsgI	GTGCAG	44	54	
BseRI	NNnnnnnnnnctcctc	48	60	(SEQ ID NO: 434)
EciI	nnnnnnnnntccgcc	52	57	(SEQ ID NO: 435)
<b>BstEII</b>	<b>Ggtnacc</b>	<b>54</b>	<b>61</b>	<b>HC Fr4, 47/79 have one</b>
EcoO109I	RGgnccy	54	86	
BpmI	ctccag	60	121	
AvaII	Ggwcc	71	140	

Please delete Table 21 and replace it with the following table:

Table 21: MALIA3, annotated

! MALIA3 9532 bases

```

! -----
! (SEQ ID NO: 451)
! 1 aat gct act act att agt aga att gat gcc acc ttt tca gct cgc gcc
! gene ii continued
! 49 cca aat gaa aat ata gct aaa cag gtt att gac cat ttg cga aat gta
! 97 tct aat ggt caa act aaa tct act cgt tcg cag aat tgg gaa tca act
! 145 gtt aca tgg aat gaa act tcc aga cac cgt act tta gtt gca tat tta
! 193 aaa cat gtt gag cta cag cac cag att cag caa tta agc tct aag cca
! 241 tcc gca aaa atg acc tct tat caa aag gag caa tta aag gta ctc tct
! 289 aat cct gac ctg ttg gag ttt gct tcc ggt ctg gtt cgc ttt gaa gct
! 337 cga att aaa acg cga tat ttg aag tct ttc ggg ctt cct ctt aat ctt
! 385 ttt gat gca atc cgc ttt gct tct gac tat aat agt cag ggt aaa gac
! 433 ctg att ttt gat tta tgg tca ttc tcg ttt tct gaa ctg ttt aaa gca
! 481 ttt gag ggg gat tca ATG aat att tat gac gat tcc gca gta ttg gac
! RBS?..... Start gene x, ii continues
! 529 gct atc cag tct aaa cat ttt act att acc ccc tct ggc aaa act tct
! 577 ttt gca aaa gcc tct cgc tat ttt ggt ttt tat cgt cgt ctg gta aac
! 625 gag ggt tat gat agt gtt gct ctt act atg cct cgt aat tcc ttt tgg
! 673 cgt tat gta tct gca tta gtt gaa tgt ggt att cct aaa tct caa ctg
! 721 atg aat ctt tct acc tgt aat aat gtt gtt ccg tta gtt cgt ttt att
! 769 aac gta gat ttt tct tcc caa cgt cct gac tgg tat aat gag cca gtt
! 817 ctt aaa atc gca TAA
! End X & II
! 832 ggtaattca ca
! (SEQ ID NO: 623)
! M1 E5 Q10 T15
! 843 ATG att aaa gtt gaa att aaa cca tct caa gcc caa ttt act act cgt
! Start gene V
! S17 S20 P25 E30
! 891 tct ggt gtt tct cgt cag ggc aag cct tat tca ctg aat gag cag ctt
! V35 E40 V45
! 939 tgt tac gtt gat ttg ggt aat gaa tat ccg gtt ctt gtc aag att act
! D50 A55 L60
! 987 ctt gat gaa ggt cag cca gcc tat gcg cct ggt cTG TAC Acc gtt cat
! BsrGI...
! L65 V70 S75 R80
! 1035 ctg tcc tct ttc aaa gtt ggt cag ttc ggt tcc ctt atg att gac cgt
! P85 K87 end of V
! 1083 ctg cgc ctc gtt ccg gct aag TAA C

```

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!
1108 ATG gag cag gtc gcg gat ttc gac aca att tat cag gcg atg
!   Start gene VII
!
1150 ata caa atc tcc gtt gta ctt tgt ttc gcg ctt ggt ata atc
!
!               VII and IX overlap.
!               ..... S2  V3  L4  V5  (SEQ ID NO: 624)      S10
1192 gct ggg ggt caa agA TGA gt gtt tta gtg tat tct ttc gcc tct ttc
gtt
!               End VII
!               |start IX
!               L13      W15      G20      T25
E29
1242 tta ggt tgg tgc ctt cgt agt ggc att acg tat ttt acc cgt tta atg
gaa
!
1293 act tcc tc
!
!       .... stop of IX, IX and VIII overlap by four bases
1301 ATG aaa aag tct tta gtc ctc aaa gcc tct gta gcc gtt gct acc ctc
!   Start signal sequence of viii.
!
1349 gtt ccg atg ctg tct ttc gct gct gag ggt gac gat ccc gca aaa gcg
!               mature VIII --->
1397 gcc ttt aac tcc ctg caa gcc tca gcg acc gaa tat atc ggt tat gcg
1445 tgg gcg atg gtt gtt gtc att
1466 gtc ggc gca act atc ggt atc aag ctg ttt aag
1499 aaa ttc acc tcg aaa gca ! 1515
!       ..... -35 ..
!
1517      agc tga taaaccgat acaattaaag gctccttttg
!               ..... -10 ...
!
1552 gagccttttt ttttGGAGAt ttt ! S.D. underlined
!
!       <----- III signal sequence ----->
!       M  K  K  L  L  F  A  I  P  L  V  (SEQ ID NO: 452)
1575 caac GTG aaa aaa tta tta ttc gca att cct tta gtt ! 1611
!
!       V  P  F  Y  S  H  S  A  Q
1612 gtt cct ttc tat tct cac aGT gcA Cag tCT
!               ApaLI...
!
1642      GTC GTG ACG CAG CCG CCC TCA GTG TCT GGG GCC CCA GGG CAG
      AGG GTC ACC ATC TCC TGC ACT GGG AGC AGC TCC AAC ATC GGG GCA
!       BstEII...
1729      GGT TAT GAT GTA CAC TGG TAC CAG CAG CTT CCA GGA ACA GCC CCC
AAA
1777      CTC CTC ATC TAT GGT AAC AGC AAT CGG CCC TCA GGG GTC CCT GAC
CGA
1825      TTC TCT GGC TCC AAG TCT GGC ACC TCA GCC TCC CTG GCC ATC ACT
1870      GGG CTC CAG GCT GAG GAT GAG GCT GAT TAT
1900      TAC TGC CAG TCC TAT GAC AGC AGC CTG AGT
1930      GGC CTT TAT GTC TTC GGA ACT GGG ACC AAG GTC ACC GTC
!               BstEII...
1969      CTA GGT CAG CCC AAG GCC AAC CCC ACT GTC ACT

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2002      CTG TTC CCG CCC TCC TCT GAG GAG CTC CAA GCC AAC AAG GCC ACA
CTA
2050      GTG TGT CTG ATC AGT GAC TTC TAC CCG GGA GCT GTG ACA GTG GCC
TGG
2098      AAG GCA GAT AGC AGC CCC GTC AAG GCG GGA GTG GAG ACC ACC ACA
CCC
2146      TCC AAA CAA AGC AAC AAC AAG TAC GCG GCC AGC AGC TAT CTG AGC
CTG
2194      ACG CCT GAG CAG TGG AAG TCC CAC AGA AGC TAC AGC TGC CAG GTC
ACG
2242      CAT GAA GGG AGC ACC GTG GAG AAG ACA GTG GCC CCT ACA GAA TGT
TCA
2290      TAA TAA ACCG CCTCCACCGG GCGCGCCAAT TCTATTTCAA GGAGACAGTC ATA
!
!                               AscI.....
!
! (SEQ ID NO: 453)
! PelB signal----->
!   M   K   Y   L   L   P   T   A   A   A   G   L   L   L   L
2343      ATG AAA TAC CTA TTG CCT ACG GCA GCC GCT GGA TTG TTA TTA CTC
!
!   16  17  18  19  20      21  22
!   A   A   Q   P   A      M   A
2388      gcG GCC cag ccG GCC      atg gcc
!
!           SfiI.....
!               NgoMI... (1/2)
!                   NcoI.....
!
!
!                               FR1 (DP47/V3-23) -----
!                               23  24  25  26  27  28  29  30
!                               E   V   Q   L   L   E   S   G
2409      gaa|gtt|CAA|TTG|tta|gag|tct|ggt|
!                               | MfeI |
!
! -----FR1-----
!   31  32  33  34  35  36  37  38  39  40  41  42  43  44  45
!   G   G   L   V   Q   P   G   G   S   L   R   L   S   C   A
2433      |ggc|ggt|ctt|gtt|cag|cct|ggt|ggt|tct|tta|cgt|ctt|tct|tgc|gct|
!
! -----FR1----->|...CDR1.....|---FR2-----
!   46  47  48  49  50  51  52  53  54  55  56  57  58  59  60
!   A   S   G   F   T   F   S   S   Y   A   M   S   W   V   R
2478      |gct|TCC|GGA|ttc|act|ttc|tct|tCG|TAC|Gct|atg|tct|tgg|gtt|cgC|
!           | BspEI |           | BsiWI |
! BstXI.
!
! -----FR2----->|...CDR2.....
!   61  62  63  64  65  66  67  68  69  70  71  72  73  74  75
!   Q   A   P   G   K   G   L   E   W   V   S   A   I   S   G
2523      |CAa|gct|cct|GGt|aaa|ggt|ttg|gag|tgg|gtt|tct|gct|atc|tct|ggt|
!           ...BstXI
!
! .....CDR2.....|---FR3---
!   76  77  78  79  80  81  82  83  84  85  86  87  88  89  90
!   S   G   G   S   T   Y   Y   A   D   S   V   K   G   R   F
2568      |tct|ggt|ggc|agt|act|tac|tat|gct|gac|tcc|gtt|aaa|ggt|cgc|ttc|
!
! -----FR3-----
!   91  92  93  94  95  96  97  98  99 100 101 102 103 104 105

```

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!       T   I   S   R   D   N   S   K   N   T   L   Y   L   Q   M
2613   |act|atc|TCT|AGA|gac|aac|tct|aag|aat|act|ctc|tac|ttg|cag|atg|
!       |   XbaI   |
!
!       ---FR3----->|
!       106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
!       N   S   L   R   A   E   D   T   A   V   Y   Y   C   A   K
2658   |aac|agC|TTA|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat|tgc|gct|aaa|
!       |AflII |           | PstI |
!
!       .....CDR3.....|-----FR4-----
!       121 122 123 124 125 126 127 128 129 130 131 132 133 134 135
!       D   Y   E   G   T   G   Y   A   F   D   I   W   G   Q   G
2703   |gac|tat|gaa|ggg|act|ggg|tat|gct|ttc|gaC|ATA|TGg|ggg|caa|ggg|
!       |           | NdeI | (1/4)
!
!       -----FR4----->|
!       136 137 138 139 140 141 142
!       T   M   V   T   V   S   S
2748   |act|atG|GTC|ACC|gtc|tct|agt
!       | BstEII |
! From BstEII onwards, pV323 is same as pCES1, except as noted.
! BstEII sites may occur in light chains; not likely to be unique in
final
! vector.
!
!
!       143 144 145 146 147 148 149 150 151 152
!       A   S   T   K   G   P   S   V   F   P
2769   gcc tcc acc aaG GGC CcA tcc GTC TTC ccc
!       Bsp120I.           BbsI... (2/2)
!       ApaI....
!
!       153 154 155 156 157 158 159 160 161 162 163 164 165 166 167
!       L   A   P   S   S   K   S   T   S   G   G   T   A   A   L
2799   ctg gca ccC TCC TCc aag agc acc tct ggg ggc aca gcg gcc ctg
!       BseRI... (2/2)
!
!       168 169 170 171 172 173 174 175 176 177 178 179 180 181 182
!       G   C   L   V   K   D   Y   F   P   E   P   V   T   V   S
2844   ggc tgc ctg GTC AAG GAC TAC TTC CCc gaA CCG GTg acg gtg tcc
!       AgeI....
!
!       183 184 185 186 187 188 189 190 191 192 193 194 195 196 197
!       W   N   S   G   A   L   T   S   G   V   H   T   F   P   A
2889   tgg aac tca GGC GCC ctg acc agc ggc gtc cac acc ttc ccg gct
!       KasI... (1/4)
!
!       198 199 200 201 202 203 204 205 206 207 208 209 210 211 212
!       V   L   Q   S   S   G   L   Y   S   L   S   S   V   V   T
2934   gtc cta cag tCt agc GGa ctc tac tcc ctc agc agc gta gtg acc
!       (Bsu36I...) (knocked out)
!
!       213 214 215 216 217 218 219 220 221 222 223 224 225 226 227
!       V   P   S   S   S   L   G   T   Q   T   Y   I   C   N   V
2979   gtg ccC tCt tct agc tTG Ggc acc cag acc tac atc tgc aac gtg
!       (BstXI.....) N.B. destruction of BstXI & BpmI
! sites.
!

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```

!      228 229 230 231 232 233 234 235 236 237 238 239 240 241 242
!      N   H   K   P   S   N   T   K   V   D   K   K   V   E   P
3024  aat cac aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc
!
!      243 244 245
!      K   S   C   A   A   A   H   H   H   H   H   H   S   A
3069  aaa tct tgt GCG GCC GCT cat cac cac cat cat cac tct gct
!      NotI.....
!
!      E   Q   K   L   I   S   E   E   D   L   N   G   A   A
3111  gaa caa aaa ctc atc tca gaa gag gat ctg aat ggt gcc gca
!
!      D   I   N   D   D   R   M   A   S   G   A
3153  GAT ATC aac gat gat cgt atg gct AGC ggc gcc
!      rEK cleavage site.....  NheI...  KsI...
!      EcoRV..
!
! Domain 1 -----
!      A   E   T   V   E   S   C   L   A
3183  gct gaa act gtt gaa agt tgt tta gca
!
!      K   P   H   T   E   IN   S   F
3210  aaa ccc cat aca gaa aat tca ttt
!
!      T   N   V   W   K   D   D   K   T
3234  aCT AAC GTC TGG AAA GAC GAC AAA Act
!
!      L   D   R   Y   A   N   Y   E   G   C   L   W   N   A   T   G
V 3261  tta gat cgt tac gct aac tat gag ggt tgt ctg tgG AAT GCT aca ggc
gtt
!
!                                     BsmI_____
!      V   V   C   T   G   D   E   T   Q   C   Y   G   T   W   V   P
I 3312  gta gtt tgt act ggt GAC GAA ACT CAG TGT TAC GGT ACA TGG GTT cct
att
!
!      G   L   A   I   P   E   N
3363  ggg ctt gct atc cct gaa aat
!
! L1 linker -----
!      E   G   G   G   S   E   G   G   G   S
3384  gag ggt ggt ggc tct gag ggt ggc ggt tct
!
!      E   G   G   G   S   E   G   G   G   T
3414  gag ggt ggc ggt tct gag ggt ggc ggt act
!
! Domain 2 -----
3444  aaa cct cct gag tac ggt gat aca cct att ccg ggc tat act tat atc
aac
3495  cct ctc gac ggc act tat ccg cct ggt act gag caa aac ccc gct aat
cct
3546  aat cct tct ctt GAG GAG tct cag cct ctt aat act ttc atg ttt cag
aat
!
!                                     BseRI___

```

```

3597 aat agg ttc cga aat agg cag ggg gca tta act gtt tat acg ggc act
3645 gtt act caa ggc act gac ccc gtt aaa act tat tac cag tac act cct
3693 gta tca tca aaa gcc atg tat gac gct tac tgg aac ggt aaa ttC AGA
!                                     AlwNI
3741 GAC TGc gct ttc cat tct ggc ttt aat gaa gat cca ttc gtt tgt gaa
!       AlwNI
3789 tat caa ggc caa tcg tct gac ctg cct caa cct cct gtc aat gct
!
3834 ggc ggc ggc tct
! start L2

```

```

-----
3846 ggt ggt ggt tct
3858 ggt ggc ggc tct
3870 gag ggt ggt ggc tct gag ggt ggc ggt tct
3900 gag ggt ggc ggc tct gag gga ggc ggt tcc
3930 ggt ggt ggc tct ggt ! end L2

```

! Domain 3

(SEQ ID NO: 454)

```

-----
!       S   G   D   F   D   Y   E   K   M   A   N   A   N   K   G   A
3945 tcc ggt gat ttt gat tat gaa aag atg gca aac gct aat aag ggg gct
!
!       M   T   E   N   A   D   E   N   A   L   Q   S   D   A   K   G
3993 atg acc gaa aat gcc gat gaa aac gcg cta cag tct gac gct aaa ggc
!
!       K   L   D   S   V   A   T   D   Y   G   A   A   I   D   G   F
4041 aaa ctt gat tct gtc gct act gat tac ggt gct gct atc gat ggt ttc
!
!       I   G   D   V   S   G   L   A   N   G   N   G   A   T   G   D
4089 att ggt gac gtt tcc ggc ctt gct aat ggt aat ggt gct act ggt gat
!
!       F   A   G   S   N   S   Q   M   A   Q   V   G   D   G   D   N
4137 ttt gct ggc tct aat tcc caa atg gct caa gtc ggt gac ggt gat aat
!
!       S   P   L   M   N   N   F   R   Q   Y   L   P   S   L   P   Q
4185 tca cct tta atg aat aat ttc cgt caa tat tta cct tcc ctc cct caa
!
!       S   V   E   C   R   P   F   V   F   S   A   G   K   P   Y   E
4233 tcg gtt gaa tgt cgc cct ttt gtc ttt agc gct ggt aaa cca tat gaa
!
!       F   S   I   D   C   D   K   I   N   L   F   R
4281 ttt tct att gat tgt gac aaa ata aac tta ttc cgt
!                                     End Domain 3
!
!
!       G   V   F   A   F   L   L   Y   V   A   T   F   M   Y   V   F140
4317 ggt gtc ttt gcg ttt ctt tta tat gtt gcc acc ttt atg tat gta ttt
!       start transmembrane segment
!
!       S   T   F   A   N   I   L
4365 tct acg ttt gct aac ata ctg
!
!       R   N   K   E   S
4386 cgt aat aag gag tct TAA ! stop of iii
!       Intracellular anchor.
!

```

(SEQ ID NO: 455)

```

!       M1  P2  V   L   L5   G   I   P   L   L10  L   R   F   L   G15

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```

4404  tc ATG cca gtt ctt ttg ggt att ccg tta tta ttg cgt ttc ctc ggt
!      Start VI
!
4451  ttc ctt ctg gta act ttg ttc ggc tat ctg ctt act ttt ctt aaa aag
4499  ggc ttc ggt aag ata gct att gct att tca ttg ttt ctt gct ctt att
4547  att ggg ctt aac tca att ctt gtg ggt tat ctc tct gat att agc gct
4595  caa tta ccc tct gac ttt gtt cag ggt gtt cag tta att ctc ccg tct
4643  aat gcg ctt ccc tgt ttt tat gtt att ctc tct gta aag gct gct att
4691  ttc att ttt gac gtt aaa caa aaa atc gtt tct tat ttg gat tgg gat
!
!      (SEQ ID NO: 456)
!      M1  A2  V3      F5      L10      G13
4739  aaa TAA t ATG gct gtt tat ttt gta act ggc aaa tta ggc tct gga
!      end VI      Start gene I
!
!      14  15  16  17  18  19  20  21  22  23  24  25  26  27  28
!      K   T   L   V   S   V   G   K   I   Q   D   K   I   V   A
4785  aag acg ctc gtt agc gtt ggt aag att cag gat aaa att gta gct
!
!      29  30  31  32  33  34  35  36  37  38  39  40  41  42  43
!      G   C   K   I   A   T   N   L   D   L   R   L   Q   N   L
4830  ggg tgc aaa ata gca act aat ctt gat tta agg ctt caa aac ctc
!
!      44  45  46  47  48  49  50  51  52  53  54  55  56  57  58
!      P   Q   V   G   R   F   A   K   T   P   R   V   L   R   I
4875  ccg caa gtc ggg agg ttc gct aaa acg cct cgc gtt ctt aga ata
!
!      59  60  61  62  63  64  65  66  67  68  69  70  71  72  73
!      P   D   K   P   S   I   S   D   L   L   A   I   G   R   G
4920  ccg gat aag cct tct ata tct gat ttg ctt gct att ggg cgc ggt
!
!      74  75  76  77  78  79  80  81  82  83  84  85  86  87  88
!      N   D   S   Y   D   E   N   K   N   G   L   L   V   L   D
4965  aat gat tcc tac gat gaa aat aaa aac ggc ttg ctt gtt ctc gat
!
!      89  90  91  92  93  94  95  96  97  98  99  100  101  102  103
!      E   C   G   T   W   F   N   T   R   S   W   N   D   K   E
5010  gag tgc ggt act tgg ttt aat acc cgt tct tgg aat gat aag gaa
!
!      104 105 106 107 108 109 110 111 112 113 114 115 116 117 118
!      R   Q   P   I   I   D   W   F   L   H   A   R   K   L   G
5055  aga cag ccg att att gat tgg ttt cta cat gct cgt aaa tta gga
!
!      119 120 121 122 123 124 125 126 127 128 129 130 131 132 133
!      W   D   I   I   F   L   V   Q   D   L   S   I   V   D   K
5100  tgg gat att att ttt ctt gtt cag gac tta tct att gtt gat aaa
!
!      134 135 136 137 138 139 140 141 142 143 144 145 146 147 148
!      Q   A   R   S   A   L   A   E   H   V   V   Y   C   R   R
5145  cag gcg cgt tct gca tta gct gaa cat gtt gtt tat tgt cgt cgt
!
!      149 150 151 152 153 154 155 156 157 158 159 160 161 162 163
!      L   D   R   I   T   L   P   F   V   G   T   L   Y   S   L
5190  ctg gac aga att act tta cct ttt gtc ggt act tta tat tct ctt
!
!      164 165 166 167 168 169 170 171 172 173 174 175 176 177 178
!      I   T   G   S   K   M   P   L   P   K   L   H   V   G   V
5235  att act ggc tgc aaa atg cct ctg cct aaa tta cat gtt ggc gtt

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!
!      179 180 181 182 183 184 185 186 187 188 189 190 191 192 193
!      V   K   Y   G   D   S   Q   L   S   P   T   V   E   R   W
! 5280 gtt aaa tat ggc gat tct caa tta agc cct act gtt gag cgt tgg
!
!      194 195 196 197 198 199 200 201 202 203 204 205 206 207 208
!      L   Y   T   G   K   N   L   Y   N   A   Y   D   T   K   Q
! 5325 ctt tat act ggt aag aat ttg tat aac gca tat gat act aaa cag
!
!      209 210 211 212 213 214 215 216 217 218 219 220 221 222 223
!      A   F   S   S   N   Y   D   S   G   V   Y   S   Y   L   T
! 5370 gct ttt tct agt aat tat gat tcc ggt gtt tat tct tat tta acg
!
!      224 225 226 227 228 229 230 231 232 233 234 235 236 237 238
!      P   Y   L   S   H   G   R   Y   F   K   P   L   N   L   G
! 5415 cct tat tta tca cac ggt cgg tat ttc aaa cca tta aat tta ggt
!
!      239 240 241 242 243 244 245 246 247 248 249 250 251 252 253
!      Q   K   M   K   L   T   K   I   Y   L   K   K   F   S   R
! 5460 cag aag atg aaa tta act aaa ata tat ttg aaa aag ttt tct cgc
!
!      254 255 256 257 258 259 260 261 262 263 264 265 266 267 268
!      V   L   C   L   A   I   G   F   A   S   A   F   T   Y   S
! 5505 gtt ctt tgt ctt gcg att gga ttt gca tca gca ttt aca tat agt
!
!      269 270 271 272 273 274 275 276 277 278 279 280 281 282 283
!      Y   I   T   Q   P   K   P   E   V   K   K   V   V   S   Q
! 5550 tat ata acc caa cct aag ccg gag gtt aaa aag gta gtc tct cag
!
!      284 285 286 287 288 289 290 291 292 293 294 295 296 297 298
!      T   Y   D   F   D   K   F   T   I   D   S   S   Q   R   L
! 5595 acc tat gat ttt gat aaa ttc act att gac tct tct cag cgt ctt
!
!      299 300 301 302 303 304 305 306 307 308 309 310 311 312 313
!      N   L   S   Y   R   Y   V   F   K   D   S   K   G   K   L
! 5640 aat cta agc tat cgc tat gtt ttc aag gat tct aag gga aaa TTA
!                                     PacI
!
!      314 315 316 317 318 319 320 321 322 323 324 325 326 327 328
!      I   N   S   D   D   L   Q   K   Q   G   Y   S   L   T   Y
! 5685 ATT AAt agc gac gat tta cag aag caa ggt tat tca ctc aca tat
!      PacI
!
!      329 330 331 332 333 334 335 336 337 338 339 340 341 342 343
!      i   I   D   L   C   T   V   S   I   K   K   G   N   S   N   E
!                                     (SEQ ID NO: 620)
!      iv                                     M1 K
! 5730 att gat tta tgt act gtt tcc att aaa aaa ggt aat tca aAT Gaa
!                                     Start IV
!
!      344 345 346 347 348 349
!      i   I   V   K   C   N   .End of I
!      iv   L3 L   N5 V   I7 N   F   V10
! 5775 att gtt aaa tgt aat TAA T TTT GTT
!      IV continued.....
! 5800 ttc ttg atg ttt gtt tca tca tct tct ttt gct cag gta att gaa atg
! 5848 aat aat tcg cct ctg cgc gat ttt gta act tgg tat tca aag caa tca
! 5896 ggc gaa tcc gtt att gtt tct ccc gat gta aaa ggt act gtt act gta

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5944 tat tca tct gac gtt aaa cct gaa aat cta cgc aat ttc ttt att tct
5992 gtt tta cgt gct aat aat ttt gat atg gtt ggt tca att cct tcc ata
6040 att cag aag tat aat cca aac aat cag gat tat att gat gaa ttg cca
6088 tca tct gat aat cag gaa tat gat gat aat tcc gct cct tct ggt ggt
6136 ttc ttt gtt cgg caa aat gat aat gtt act caa act ttt aaa att aat
6184 aac gtt cgg gca aag gat tta ata cga gtt gtc gaa ttg ttt gta aag
6232 tct aat act tct aaa tcc tca aat gta tta tct att gac ggc tct aat
6280 cta tta gtt gtt TCT gca cct aaa gat att tta gat aac ctt cct caa
!
6328 ttc ctt tct act gtt gat ttg cca act gac cag ata ttg att gag ggt
6376 ttg ata ttt gag gtt cag caa ggt gat gct tta gat ttt tca ttt gct
6424 gct ggc tct cag cgt ggc act gtt gca ggc ggt gtt aat act gac cgc
6472 ctc acc tct gtt tta tct tct gct ggt ggt tct ttc ggt att ttt aat
6520 ggc gat gtt tta ggg cta tca gtt cgc gca tta aag act aat agc cat
6568 tca aaa ata ttg tct gtg cca cgt att ctt acg ctt tca ggt cag aag
6616 ggt tct atc tct gtT GGC CAG aat gtc cct ttt att act ggt cgt gtg
!
6664 act ggt gaa tct gcc aat gta aat aat cca ttt cag acg att gag cgt
6712 caa aat gta ggt att tcc atg agc gtt ttt cct gtt gca atg gct ggc
6760 ggt aat att gtt ctg gat att acc agc aag gcc gat agt ttg agt tct
6808 tct act cag gca agt gat gtt att act aat caa aga agt att gct aca
6856 acg gtt aat ttg cgt gat gga cag act ctt tta ctc ggt ggc ctc act
6904 gat tat aaa aac act tct caa gat tct ggc gta ccg ttc ctg tct aaa
6952 atc cct tta atc ggc ctc ctg ttt agc tcc cgc tct gat tcc aac gag
7000 gaa agc acg tta tac gtg ctc gtc aaa gca acc ata gta cgc gcc ctg
7048 TAG cggcgcatt
!
7060 aagcgcggcg ggtgtggtgg ttacgcgcag cgtgaccgct acacttgcca
gcgccttagc
7120 gccgcgtcct ttcgctttct tcccttcctt tctcgccacg ttcGCCGGCt
ttccccgtca
!
7180 agctctaaat cgggggctcc ctttaggggt ccgatttagt gctttacggc
acctcgaccc
7240 caaaaaactt gatttggtg atgggtCACG TAGTGggcca tcgccctgat
agacggtttt
!
7300 tcgccctttG ACGTTGGAGT Ccactgtctt taatagtga ctcttggtcc
aaactggaac
!
7360 aacactcaac cctatctcgg gctattcttt tgatttataa gggattttgc
cgatttcgga
7420 accaccatca aacaggattt tcgcctgctg gggcaaacca gcgtggaccg
cttgctgcaa
7480 ctctctcagg gccaggcggg gaagggaat CAGCTGttgc cCGTCTCact
ggtgaaaaga
!
7540 aaaaccaccc tGGATCC AAGCTT
!
BamHI HindIII (½)
PvuII. BsmBI.

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```

!               Insert carrying bla gene
7563      gcaggtg gcacttttcg gggaaatgtg cgcggaaccc
7600 ctatttggtt atttttctaa atacattcaa atatGTATCC gctcatgaga
caataaccct
!
!               BciVI
7660 gataaatgct tcaataatat tgaaaaAGGA AGAgt
!               RBS.?...
!
!       Start bla gene
7695 ATG agt att caa cat ttc cgt gtc gcc ctt att ccc ttt ttt gcg gca
ttt
7746 tgc ctt cct gtt ttt gct cac cca gaa acg ctg gtg aaa gta aaa gat
gct
7797 gaa gat cag ttg ggC gCA CGA Gtg ggt tac atc gaa ctg gat ctc aac
agc
!
!               BssSI...
!               ApaLI removed
7848 ggt aag atc ctt gag agt ttt cgc ccc gaa gaa cgt ttt cca atg atg
agc
7899 act ttt aaa gtt ctg cta tgt cat aca cta tta tcc cgt att gac gcc
ggg
7950 caa gaG CAA CTC GGT CGc cgg gcg cgg tat tct cag aat gac ttg gtt
gAG
!
!               BcgI_____
ScaI
8001 TAC Tca cca gtc aca gaa aag cat ctt acg gat ggc atg aca gta aga
gaa
!
!               ScaI_____
8052 tta tgc agt gct gcc ata acc atg agt gat aac act gcg gcc aac tta
ctt
8103 ctg aca aCG ATC Gga gga ccg aag gag cta acc gct ttt ttg cac aac
atg
!
!               PvuI_____
8154 ggg gat cat gta act cgc ctt gat cgt tgg gaa ccg gag ctg aat gaa
gcc
8205 ata cca aac gac gag cgt gac acc acg atg cct gta gca atg cca aca
acg
8256 tTG CGC Aaa cta tta act ggc gaa cta ctt act cta gct tcc cgg caa
caa
!
!               FspI....
!
8307 tta ata gac tgg atg gag gcg gat aaa gtt gca gga cca ctt ctg cgc
tcg
8358 GCC ctt ccG GcT ggc tgg ttt att gct gat aaa tct gga gcc ggt gag
cgt
!
!               BglI_____
8409 gGG TCT Cgc ggt atc att gca gca ctg ggg cca gat ggt aag ccc tcc
cgt
!
!               BsaI_____
8460 atc gta gtt atc tac acG ACg ggg aGT Cag gca act atg gat gaa cga
aat
!
!               AhdI_____
8511 aga cag atc gct gag ata ggt gcc tca ctg att aag cat tgg TAA ctgt
!               stop
8560 cagaccaagt ttactcatat atactttaga ttgatttaaa acttcatttt
taatttaaaa
8620 ggatctagggt gaagatcctt tttgataatc tcatgaccaa aatcccttaa
cgtgagtttt
8680 cgttccactg tacgtaagac cccc

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8704 AAGCTT   GTCGAC tgaa tggcgaatgg cgctttgcct
!      HindIII  SalI..
!      (2/2)    HincII
8740 ggttttccggc accagaagcg gtgcgggaaa gctggctgga gtgcgatctt
!
8790 CCTGAGG
!      Bsu36I_
8797      ccgat actgtcgtcg tccctcaaa ctggcagatg
8832 cacggttacg atgcgcccat ctacaccaac gtaacctatc ccattacggt
caatccgccg
8892 tttgttccca cggagaatcc gacgggttgt tactcgctca catttaatgt
tgatgaaagc
8952 tggctacagg aaggccagac gcgaattatt tttgatggcg ttcctattgg
ttaaaaaatg
9012 agctgattta acaaaaattht aacgcgaatt ttaacaaaat attaacgttt
acaATTTAAA
!
SwaI...
9072 Tatttgetta tacaatcttc ctgtttttgg ggcttttctg attatcaacc GGGGTAcac
!                                     RBS?
9131 ATG att gac atg cta gtt tta cga tta ccg ttc atc gat tct ctt gtt
tgc
!      Start gene II
9182 tcc aga ctc tca ggc aat gac ctg ata gcc ttt gtA GAT CTc tca aaa
ata
!
!                                     BglII...
9233 gct acc ctc tcc ggc atg aat tta tca gct aga acg gtt gaa tat cat
att
9284 gat ggt gat ttg act gtc tcc ggc ctt tct cac cct ttt gaa tct tta
cct
9335 aca cat tac tca ggc att gca ttt aaa ata tat gag ggt tct aaa aat
ttt
9386 tat cct tgc gtt gaa ata aag gct tct ccc gca aaa gta tta cag ggt
cat
9437 aat gtt ttt ggt aca acc gat tta gct tta tgc tct gag gct tta ttg
ctt
9488 aat ttt gct aat tct ttg cct tgc ctg tat gat tta ttg gat gtt !
9532
! gene II continues

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Please delete Table 21B and replace it with the following table:

Table 21B: Sequence of MALIA3, condensed

LOCUS	MALIA3		9532	CIRCULAR		
ORIGIN						
(SEQ ID NO: 451)						
1	AATGCTACTA	CTATTAGTAG	AATTGATGCC	ACCTTTTTCAG	CTCGCGCCCC	AAATGAAAAT
61	ATAGCTAAAC	AGGTTATTGA	CCATTTGCGA	AATGTATCTA	ATGGTCAAAC	TAAATCTACT
121	CGTTGCGAGA	ATTGGGAATC	AACTGTTACA	TGGAATGAAA	CTTCCAGACA	CCGTACTTTA
181	GTTGCATATT	TAAAACATGT	TGAGCTACAG	CACCAGATTC	AGCAATTAAG	CTCTAAGCCA
241	TCCGCAAAAA	TGACCTCTTA	TCAAAAGGAG	CAATTAAAGG	TACTCTCTAA	TCCTGACCTG
301	TTGGAGTTTG	CTTCCGGTCT	GGTTCGCTTT	GAAGCTCGAA	TTAAAACGCG	ATATTTGAAG
361	TCTTTCGGGC	TTCTCTTTAA	TCTTTTTTGT	GCAATCCGCT	TTGCTTCTGA	CTATAATAGT
421	CAGGGTAAAG	ACCTGATTTT	TGATTTATGAT	TCATTCTCGT	TTTCTGAACT	GTTTAAAGCA
481	TTTGAGGGGG	ATTCAATGAA	TATTTATGAC	GATTTCCGAG	TATTGGACGC	TATCCAGTCT
541	AAACATTTTA	CTATTACCCC	CTCTGGCAAA	ACTTCTTTTG	CAAAAGCCTC	TCGCTATTTT
601	GGTTTTTATC	GTCGTCTGGT	AAACGAGGGT	TATGATAGTG	TTGCTCTTAC	TATGCCTCGT
661	AATTCCTTTT	GGCGTTATGT	ATCTGCATTA	GTTGAATGTG	GTATTCTTAA	ATCTCAACTG
721	ATGAATCTTT	CTACCTGTAA	TAATGTTGTT	CCGTTAGTTC	GTTTTATTAA	CGTAGATTTT
781	TCTTCCCAAC	GTCTGACTG	GTATAATGAG	CCAGTTCTTA	AAATCGCATA	AGGTAATTCA
841	CAATGATTAA	AGTTGAAATT	AAACCATCTC	AAGCCCAATT	TACTACTCGT	TCTGGTGTTT
901	CTCGTCAGGG	CAAGCCTTAT	TCACTGAATG	AGCAGCTTTG	TTACGTTGAT	TTGGGTAATG
961	AATATCCGGT	TCTTGTCAAG	ATTACTCTTG	ATGAAGGTCA	GCCAGCCTAT	GCGCCTGGTC
1021	TGTACACCGT	TCATCTGTCC	TCTTTCAAAG	TTGGTCAGTT	CGGTTCCCTT	ATGATTGACC
1081	GTCTGCGCCT	CGTTCGGGCT	AAGTAACATG	GAGCAGGTCG	CGGATTTTCA	CACAATTTAT
1141	CAGGCGATGA	TACAAATCTC	CGTTGTACTT	TGTTTCGCGC	TTGGTATAAT	CGCTGGGGGT
1201	CAAAGATGAG	TGTTTTAGTG	TATTCCTTTC	CCTCTTTTCG	TTTAGGTTGG	TGCCTTCGTA
1261	GTGGCATTAC	GTATTTTACC	CGTTTAATGG	AAACTTCCTC	ATGAAAAAGT	CTTTAGTCCT
1321	CAAAGCCTCT	GTAGCCGTTG	CTACCCTCGT	TCCGATGCTG	TCTTTCGCTG	CTGAGGGTGA
1381	CGATCCCGCA	AAAGCGGCCT	TTAACTCCCT	GCAAGCCTCA	GCGACCGAAT	ATATCGGTTA
1441	TGCGTGGGCG	ATGGTTGTTG	TCATTGTCCG	CGCAACTATC	GGTATCAAGC	TGTTTAAGAA
1501	ATTCACCTCG	AAAGCAAGCT	GATAAACCGA	TACAATTAAA	GGCTCCTTTT	GGAGCCTTTT
1561	TTTTTGAGAG	TTTTCAACGT	GAAAAAATTA	TTATTCGCAA	TTCCTTTAGT	TGTTCCTTTC
1621	TATTCTCACA	GTGCACAGTC	TGTCGTGACG	CAGCCGCCCT	CAGTGTCTGG	GGCCCCAGGG
1681	CAGAGGGTCA	CCATCTCCTG	CACTGGGAGC	AGCTCCAACA	TCGGGGCAGG	TTATGATGTA
1741	CACTGGTACC	AGCAGCTTCC	AGGAACAGCC	CCCAAACCTC	TCATCTATGG	TAACAGCAAT
1801	CGGCCCTCAG	GGGTCCCTGA	CCGATTCTCT	GGCTCCAAGT	CTGGCACCTC	AGCCTCCCTG
1861	GCCATCACTG	GGCTCCAGGC	TGAGGATGAG	GCTGATTATT	ACTGCCAGTC	CTATGACAGC
1921	AGCCTGAGTG	GCCTTTATGT	CTTCGGAAC	GGGACCAAGG	TCACCGTCCT	AGGTCAGCCC
1981	AAGGCCAACC	CCACTGTCAC	TCTGTTCCCG	CCCTCCTCTG	AGGAGCTCCA	AGCCAACAAG
2041	GCCACACTAG	TGTGTCTGAT	CAGTGAATTC	TACCCGGGAG	CTGTGACAGT	GGCCTGGAAG
2101	GCAGATAGCA	GCCCCGTCAA	GGCGGGAGTG	GAGACCACCA	CACCCTCCAA	ACAAAGCAAC
2161	AACAAGTACG	CGGCCAGCAG	CTATCTGAGC	CTGACGCCTG	AGCAGTGGA	GTCCACAGA
2221	AGCTACAGCT	GCCAGGTCAC	GCATGAAGGG	AGCACCGTGG	AGAAGACAGT	GGCCCCTACA
2281	GAATGTTTAT	AATAAACCGC	CTCCACCGGG	CGCGCCAATT	CTATTTCAAG	GAGACAGTCA
2341	TAATGAAATA	CCTATTGCCT	ACGGCAGCCG	CTGGATTGTT	ATTACTCGCG	GCCCAGCCGG
2401	CCATGGCCGA	AGTTCAATTG	TTAGAGTCTG	GTGGCGGTCT	TGTTTACGCT	GGTGGTTCCT
2461	TACGTCTTTC	TTGCGCTGCT	TCCGGATTCA	CTTTCTCTTC	GTACGCTATG	TCTTGGGTTC
2521	GCCAAGCTCC	TGGTAAAGGT	TTGGAGTGGG	TTTCTGCTAT	CTCTGGTTCT	GGTGGCAGTA
2581	CTTACTATGC	TGACTCCGTT	AAAGGTCGCT	TCACTATCTC	TAGAGACAAC	TCTAAGAATA
2641	CTCTCTACTT	GCAGATGAAC	AGCTTAAGGG	CTGAGGACAC	TGCAGTCTAC	TATTGCGCTA
2701	AAGACTATGA	AGGTACTGGT	TATGCTTTTC	ACATATGGGG	TCAAGGTACT	ATGGTCACCG
2761	TCTCTAGTGC	CTCCACCAAG	GGCCCATCGG	TCTTCCCCCT	GGCACCCCTC	TCCAAGAGCA
2821	CCTCTGGGGG	CACAGCGGCC	CTGGGCTGCG	TGGTCAAGGA	CTACTTCCCC	GAACCGGTGA
2881	CGGTGTCGTG	GAACTCAGGC	GCCCTGACCA	GCGGCGTCCA	CACCTTCCCC	GCTGTCTTAC
2941	AGTCTAGCGG	ACTCTACTCC	CTCAGCAGCG	TAGTGACCGT	GCCCTCTTCT	AGCTTGGGCA
3001	CCCAGACCTA	CATCTGCAAC	GTGAATCACA	AGCCCAGCAA	CACCAAGGTG	GACAAGAAAG

3061	TTGAGCCCAA	ATCTTGTGCG	GCCGCTCATC	ACCACCATCA	TCACTCTGCT	GAACAAAAAC
3121	TCATCTCAGA	AGAGGATCTG	AATGGTGCCG	CAGATATCAA	CGATGATCGT	ATGGCTGGCG
3181	CCGCTGAAAC	TGTTGAAAGT	TGTTTAGCAA	AACCCCATAC	AGAAAATTCA	TTTACTAACG
3241	TCTGGAAAGA	CGACAAAAC	TTAGATCGTT	ACGCTAACTA	TGAGGGTTGT	CTGTGGAATG
3301	CTACAGGCGT	TGTAGTTTGT	ACTGGTGACG	AAACTCAGTG	TTACGGTACA	TGGGTTCCCTA
3361	TTGGGCTTGC	TATCCCTGAA	AATGAGGGTG	GTGGCTCTGA	GGGTGGCGGT	TCTGAGGGTG
3421	GCGGTTCTGA	GGGTGGCGGT	ACTAAACCTC	CTGAGTACGG	TGATACACCT	ATTCCGGGCT
3481	ATACTTATAT	CAACCCTCTC	GACGGCACTT	ATCCGCCTGG	TACTGAGCAA	AACCCCGCTA
3541	ATCCTAATCC	TTCTCTTGAG	GAGTCTCAGC	CTCTTAATAC	TTTCATGTTT	CAGAATAATA
3601	GGTTCCGAAA	TAGGCAGGGG	GCATTAAC	TTTATACGGG	CACTGTTACT	CAAGGCACTG
3661	ACCCCGTTAA	AACTTATTAC	CAGTACACTC	CTGTATCATC	AAAAGCCATG	TATGACGCTT
3721	ACTGGAACGG	TAAATTCAGA	GACTGCGCTT	TCCATTCTGG	CTTTAATGAA	GATCCATTCTG
3781	TTTGTGAATA	TCAAGGCCAA	TCGTCTGACC	TGCCTCAACC	TCCTGTCAAT	GCTGGCGGCG
3841	GCTCTGGTGG	TGGTTCTGGT	GGCGGCTCTG	AGGGTGGTGG	CTCTGAGGGT	GGCGGTTCTG
3901	AGGGTGGCGG	CTCTGAGGGA	GGCGGTTCCG	GTGGTGGCTC	TGGTTCCGGT	GATTTTGATT
3961	ATGAAAAGAT	GGCAAACGCT	AATAAGGGGG	CTATGACCGA	AAATGCCGAT	GAAAACGCGC
4021	TACAGTCTGA	CGCTAAAGGC	AACTTGATT	CTGTCGCTAC	TGATTACGGT	GCTGCTATCG
4081	ATGGTTTCAT	TGGTGACGTT	TCCGGCCTTG	CTAATGGTAA	TGGTGCTACT	GGTGATTTTG
4141	CTGGCTCTAA	TTCCCAAATG	GCTCAAGTCG	GTGACGGTGA	TAATTCACCT	TTAATGAATA
4201	ATTTCCGTCA	ATATTTACCT	TCCCTCCCTC	AATCGGTTGA	ATGTCGCCCT	TTTGTCTTTA
4261	GCGTGGTAA	ACCATATGAA	TTTTCTATTG	ATTGTGACAA	AATAAACTTA	TTCCGTGGTG
4321	TCTTTGCGTT	TCTTTTATAT	TGTGCCACCT	TTATGTATGT	ATTTTCTACG	TTTGCTAACA
4381	TACTGCGTAA	TAAGGAGTCT	TAATCATGCC	AGTTCTTTTG	GGTATTCGGT	TATTATTGCG
4441	TTTCCTCGGT	TTCTTCTGG	TAACCTTTGTT	CGGCTATCTG	CTTACTTTTC	TTAAAAAGGG
4501	CTTCGGTAAG	ATAGCTATTG	CTATTTTCA	GTTTCTTGCT	CTTATTATTG	GGCTTAACTC
4561	AATTCTTG	GGTTATCTCT	CTGATATTAG	CGCTCAATTA	CCCTCTGACT	TTGTTCAAGG
4621	TGTTCAAGTTA	ATTCTCCCGT	CTAATGCGCT	TCCCTGTTTT	TATGTTATTC	TCTCTGTAAA
4681	GGCTGCTATT	TTCAATTTTG	ACGTTAAACA	AAAAATCGTT	TCTTATTTTG	ATTGGGATAA
4741	ATAATATGGC	TGTTTATTTT	GTAAGTGGCA	AATTAGGCTC	TGGAAAGACG	CTCGTTAGCG
4801	TTGGTAAGAT	TCAGGATAAA	ATTGTAGCTG	GGTGCAAAAT	AGCAACTAAT	CTTGATTTAA
4861	GGCTTCAAAA	CCTCCCGCAA	GTCGGGAGGT	TCGCTAAAAC	GCCTCGCGTT	CTTAGAATAC
4921	CGGATAAGCC	TTCTATATCT	GATTTGCTTG	CTATTGGGCG	CGGTAATGAT	TCCTACGATG
4981	AAAATAAAAA	CGGCTTGCTT	GTTCTCGATG	AGTGCGGTAC	TTGGTTTAA	ACCCGTTCTT
5041	GGAATGATAA	GGAAAGACAG	CCGATTATTG	ATTGGTTTCT	ACATGCTCGT	AAATTAGGAT
5101	GGGATATTAT	TTTTCTTGTT	CAGGACTTAT	TATTGTGTTGA	TAAACAGGCG	CGTTCTGCAT
5161	TAGCTGAACA	TGTTGTTTAT	TGTCGTCGTC	TGGACAGAAT	TACTTTACCT	TTTGTCGGTA
5221	TTTTATATTC	TCTTATTACT	GGCTCGAAAA	TGCCTCTGCC	TAAATTACAT	TTTGGCGTTG
5281	TTAAATATGG	CGATTCTCAA	TTAAGCCCTA	CTGTTGAGCG	TTGGCTTTAT	ACTGGTAAGA
5341	ATTTGTATAA	CGCATATGAT	ACTAAACAGG	CTTTTTCTAG	TAATTATGAT	TCCGGTGTTT
5401	ATTCCTATTT	AACGCCTTAT	TTATCACACG	GTCGGTATTT	CAAACCATTA	AATTTAGGTC
5461	AGAAGATGAA	ATTAAGTAAA	ATATATTTGA	AAAAGTTTTT	TCGCGTTCTT	TGTCTTGCGA
5521	TTGGATTG	ATCAGCATTT	ACATATAGTT	ATATAACCCA	ACCTAAGCCG	GAGGTTAAAA
5581	AGGTAGTCTC	TCAGACCTAT	GATTTTGATA	AATTCACAT	TGACTCTTCT	CAGCGTCTTA
5641	ATCTAAGCTA	TCGCTATGTT	TTCAAGGATT	CTAAGGGAAA	ATTAATTAAT	AGCGACGATT
5701	TACAGAAGCA	AGGTTATTCA	CTCACATATA	TTGATTATG	TACTGTTTCC	ATTAATAAAG
5761	GTAATTCAAA	TGAAATTGTT	AAATGTAATT	AATTTTGTTT	TCTTGATGTT	TGTTTCATCA
5821	TCTTCTTTTG	CTCAGGTAAT	TGAAATGAAT	AATTCGCCTC	TGCGCGATTT	TGTAAGTTGG
5881	TATTCAAAGC	AATCAGGCGA	ATCCGTTATT	GTTTCTCCCG	ATGTAAAAGG	TACTGTTACT
5941	GTATATTCAT	CTGACGTTAA	ACCTGAAAA	CTACGCAATT	TCTTTATTTT	TGTTTTACGT
6001	GCTAATAATT	TTGATATGGT	TGGTTCAATT	CCTTCCATAA	TTCAGAAGTA	TAATCCAAAC
6061	AATCAGGATT	ATATTGATGA	ATTGCCATCA	TCTGATAATC	AGGAATATGA	TGATAATTCC
6121	GCTCCTTCTG	GTGGTTTCTT	TGTTCCGCAA	AATGATAATG	TTACTCAAAC	TTTAAAAATT
6181	AATAACGTTT	GGGCAAAGGA	TTTAATACGA	GTTGTCGAAT	TGTTTGTA	GTCTAATACT
6241	TCTAAATCCT	CAAATGTATT	ATCTATTGAC	GGCTCTAATC	TATTAGTTGT	TTCTGCACCT
6301	AAAGATATTT	TAGATAACCT	TCCTCAATTC	CTTTCTACTG	TTGATTTGCC	AACTGACCAG
6361	ATATTGATTG	AGGGTTTGAT	ATTTGAGGTT	CAGCAAGGTG	ATGCTTTAGA	TTTTTCATTT
6421	GCTGCTGGCT	CTCAGCGTGG	CACTGTTGCA	GGCGGTGTTA	ATACTGACCG	CCTCACCTCT
6481	GTTTTATCTT	CTGCTGGTGG	TTCGTTCCGT	ATTTTAAATG	GCGATGTTTT	AGGGCTATCA

6541	GTTCGCGCAT	TAAAGACTAA	TAGCCATTCA	AAAATATTGT	CTGTGCCACG	TATTCTTACG
6601	CTTTCAGGTC	AGAAGGGTTC	TATCTCTGTT	GGCCAGAATG	TCCCTTTTAT	TACTGGTTCGT
6661	GTGACTGGTG	AATCTGCCAA	TGTAAATAAT	CCATTTTCAGA	CGATTGAGCG	TCAAAATGTA
6721	GGTATTTCCA	TGAGCGTTTT	TCCTGTTGCA	ATGGCTGGCG	GTAATATTGT	TCTGGATATT
6781	ACCAGCAAGG	CCGATAGTTT	GAGTTCTTCT	ACTCAGGCAA	GTGATGTTAT	TACTAATCAA
6841	AGAAGTATTG	CTACAACGGT	TAATTTGCGT	GATGGACAGA	CTCTTTTACT	CGGTGGCCTC
6901	ACTGATTATA	AAAACACTTC	TCAAGATTCT	GGCGTACCGT	TCCTGTCTAA	AATCCCTTTA
6961	ATCGGCCTCC	TGTTTAGCTC	CCGCTCTGAT	TCCAACGAGG	AAAGCACGTT	ATACGTGCTC
7021	GTCAAAGCAA	CCATAGTACG	CGCCCTGTAG	CGGCGCATT	AGCGCGGCGG	GTGTGGTGGT
7081	TACGCGCAGC	GTGACCGCTA	CACCTGCCAG	CGCCCTAGCG	CCCGCTCCTT	TCGCTTTCTT
7141	CCCTTCCTTT	CTCGCCACGT	TCGCCGGCTT	TCCCCGTCAA	GCTCTAAATC	GGGGGCTCCC
7201	TTTAGGGTTC	CGATTTAGTG	CTTTACGGCA	CCTCGACCCC	AAAAAACTTG	ATTTGGGTGA
7261	TGGTTCACGT	AGTGGGCCAT	CGCCCTGATA	GACGGTTTTT	CGCCCTTTGA	CGTTGGAGTC
7321	CACGTTCTTT	AATAGTGGAC	TCTTGTTCCA	AACTGGAACA	ACACTCAACC	CTATCTCGGG
7381	CTATTCTTTT	GATTTATAAG	GGATTTTGCC	GATTTTCGGAA	CCACCATCAA	ACAGGATTTT
7441	CGCCTGCTGG	GGCAAACCAG	CGTGGACCGC	TTGCTGCAAC	TCTCTCAGGG	CCAGGCGGTG
7501	AAGGGCAATC	AGCTGTTGCC	CGTCTCACTG	GTGAAAAGAA	AAACCACCTT	GGATCCAAGC
7561	TTGCAGGTGG	CACTTTTCGG	GGAAATGTGC	GCGGAACCCC	TATTTGTTTA	TTTTTCTAAA
7621	TACATTCAAA	TATGTATCCG	CTCATGAGAC	AATAACCCTG	ATAAATGCTT	CAATAATATT
7681	GAAAAAGGAA	GAGTATGAGT	ATTCAACATT	TCCGTGTCGC	CCTTATTCCC	TTTTTTGCGG
7741	CATTTTGCCT	TCCTGTTTTT	GCTCACCCAG	AAACGCTGGT	GAAAGTAAAA	GATGCTGAAG
7801	ATCAGTTGGG	CGCACGAGTG	GGTTACATCG	AACCTGGATCT	CAACAGCGGT	AAGATCCTTG
7861	AGAGTTTTTCG	CCCCGAAGAA	CGTTTTTCCAA	TGATGAGCAC	TTTTAAAGTT	TCTCTATGTC
7921	ATACACTATT	ATCCCGTATT	GACGCCGGGC	AAGAGCAACT	CGGTCGCCGG	GCGCGGTATT
7981	CTCAGAAATGA	CTTGTTTGAG	TACTCACCAG	TCACAGAAAA	GCATCTTACG	GATGGCATGA
8041	CAGTAAGAGA	ATTATGCAGT	GCTGCCATAA	CCATGAGTGA	TAACACTGCG	GCCAACTTAC
8101	TTCTGACAAC	GATCGGAGGA	CCGAAGGAGC	TAACCGCTTT	TTTGCACAAC	ATGGGGGATC
8161	ATGTAACCTG	CCTTGATCGT	TGGGAACCGG	AGCTGAATGA	AGCCATACCA	AACGACGAGC
8221	GTGACACCAC	GATGCCTGTA	GCAATGCCAA	CAACGTTGCG	CAAACCTATTA	ACTGGCGAAC
8281	TACTTACTCT	AGCTTCCCGG	CAACAATTAA	TAGACTGGAT	GGAGGCGGAT	AAAGTTGCAG
8341	GACCACTTCT	GCGCTCGGCC	CTTCCGGCTG	GCTGGTTTAT	TGCTGATAAA	TCTGGAGCCG
8401	GTGAGCGTGG	GTCTCGCGGT	ATCATTGCAG	CACTGGGGCC	AGATGGTAAG	CCCTCCCGTA
8461	TCGTAGTTAT	CTACACGACG	GGGAGTCAGG	CAACTATGGA	TGAACGAAAT	AGACAGATCG
8521	CTGAGATAGG	TGCCTCACTG	ATTAAGCATT	GGTAACTGTC	AGACCAAGTT	TACTCATATA
8581	TACTTTAGAT	TGATTTAAAA	CTTCATTTT	AATTTAAAAG	GATCTAGGTG	AAGATCCTTT
8641	TTGATAATCT	CATGACCAAA	ATCCCTTAAC	GTGAGTTTTC	GTTCCACTGT	ACGTAAGACC
8701	CCCAAGCTTG	TCGACTGAAT	GGCGAATGGC	GCTTTGCCCTG	GTTTCCGGCA	CCAGAAGCGG
8761	TGCCGGAAAG	CTGGCTGGAG	TGCGATCTTC	CTGAGGCCGA	TACTGTCGTC	GTCCCTCAA
8821	ACTGGCAGAT	GCACGGTTAC	GATGCGCCCA	TCTACACCAA	CGTAACCTAT	CCCATTACGG
8881	TCAATCCGCC	GTTTGTTCCC	ACGGAGAATC	CGACGGGTG	TTACTCGCTC	ACATTTAATG
8941	TTGATGAAAG	CTGGCTACAG	GAAGGCCAGA	CGCGAATTAT	TTTTGATGGC	GTTCCATTG
9001	GTTAAAAAAT	GAGCTGATTT	AACAAAAATT	TAACGCGAAT	TTTAACAAAA	TATTAACGTT
9061	TACAATTTAA	ATATTGCTT	ATACAATCTT	CCTGTTTTTG	GGGCTTTTCT	GATTATCAAC
9121	CGGGGTACAT	ATGATTGACA	TGCTAGTTTT	ACGATTACCG	TTTCATCGATT	CTCTTGTTTG
9181	CTCCAGACTC	TCAGGCAATG	ACCTGATAGC	CTTTGTAGAT	CTCTCAAAAA	TAGCTACCCT
9241	CTCCGGCATG	AATTTATCAG	CTAGAACGGT	TGAATATCAT	ATTGATGGTG	ATTTGACTGT
9301	CTCCGGCCTT	TCTCACCTT	TTGAATCTTT	ACCTACACAT	TACTCAGGCA	TTGCATTTAA
9361	AATATATGAG	GGTTCTAAAA	ATTTTTATCC	TTGCGTTGAA	ATAAAGGCTT	CTCCCGCAAA
9421	AGTATTACAG	GGTCATAATG	TTTTTGCTAC	AACCGATTTA	GCTTTATGCT	CTGAGGCTTT
9481	ATTGCTTAAT	TTTGCTAATT	CTTTGCCTTG	CCTGTATGAT	TTATTGGATG	TT

Please delete Table 22 and replace it with the following table:

Table 22: Primers used in RACE amplification:

Heavy chain	
HuCμ-FOR (1st PCR)	5'-TGG AAG AGG CAC GTT CTT TTC TTT-3' (SEQ ID NO: 457)
HuCμ-Nested (2nd PCR)	5' CTT TTC TTT GTT GCC GTT GGG GTG-3' (SEQ ID NO: 458)
Kappa light chain	
HuκkFor (1st PCR)	5'-ACA CTC TCC CCT GTT GAA GCT CTT-3' (SEQ ID NO: 459)
HuκkForAscI(2nd PCR)	5'-ACC GCC TCC ACC GGG CGC GGC TTA TTA ACA CTC TCC CCT GTT GAA GCT CTT-3' (SEQ ID NO: 460)
Lambda light chain	
HuλambdaFor (1st PCR)	5'-TGA ACA TTC TGT AGG GGC CAC TG-3' (SEQ ID NO: 461)
HuCL2-FOR	5'-AGA GCA TTC TGC AGG GGC CAC TG-3' (SEQ ID NO: 462)
HuλambdaForAscI (2nd PCR)	
HuCL2-FOR-ASC	5'-ACC GCC TCC ACC GGG CGC GCC TTA TTA TGA ACA TTC TGT AGG GGC CAC TG-3' (SEQ ID NO: 463)
HuCL7-FOR-ASC	5'-ACC GCC TCC ACC GGG CGC GCC TTA TTA AGA GCA TTC TGC AGG GGC CAC TG-3' (SEQ ID NO: 464)
GeneRacer 5' Primers provided with the kit (Invitrogen)	
5'A 1st PCR	(SEQ ID NO: 465) 5'CGACTGGAGCACGAGGACACTGA 3'
5'NA 2nd pCR	5'GGACACTGACATGGACTGAAGGAGTA-3' (SEQ ID NO: 466)

Please delete Table 23 and replace it with the following table:

Table 23: ONs used in Capture of kappa light chains using CJ method and BsmAI

All ONs are written 5' to 3'.

Redapters (6)	
ON_20SK15012	gggAggATggAgAcTgggTc (SEQ ID NO: 467)
ON_20SK15L12	gggAAGATggAgAcTgggTc (SEQ ID NO: 468)
ON_20SK15A17	gggAgAgTggAgAcTgAgTc (SEQ ID NO: 469)
ON_20SK15A27	gggTgccTggAgAcTgcgTc (SEQ ID NO: 470)
ON_20SK15A11	gggTggcTggAgAcTgcgTc (SEQ ID NO: 471)
ON_20SK15B3	gggAgTcTggAgAcTgggTc (residues 1-20 of SEQ ID NO: 477)

Bridges (6)	
kapbril012	gggAggATggAgAcTgggTcATcTggATgTcTTgTgcAcTgTgAcAgAgg (SEQ ID NO: 472)
kapbrilL12	gggAAGATggAgAcTgggTcATcTggATgTcTTgTgcAcTgTgAcAgAgg (SEQ ID NO: 473)
kapbrilA17	gggAgAgTggAgAcTgggTcATcTggATgTcTTgTgcAcTgTgAcAgAgg (SEQ ID NO: 474)
kapbrilA27	gggTgccTggAgAcTgggTcATcTggATgTcTTgTgcAcTgTgAcAgAgg (SEQ ID NO: 475)
kapbrilA11	gggTggcTggAgAcTgggTcATcTggATgTcTTgTgcAcTgTgAcAgAgg (SEQ ID NO: 476)
kapbrilB3	gggAgTcTggAgAcTgggTcATcTggATgTcTTgTgcAcTgTgAcAgAgg (SEQ ID NO: 477)

Extender (5' biotinylated)  
kapextlbio ccTcTgTcAcAgTgcAcAAgAcATccAgATgAcccAgTcTcc (SEQ ID NO: 478)

Primers  
kaPCRtl ccTcTgTcAcAgTgcAcAAgAc (SEQ ID NO: 479)  
kapfor 5'-aca ctc tcc cct gtt gaa gct ctt-3' (SEQ ID NO: 480)



Please delete Table 25 and replace it with the following table:

Table 25: h3401-h2 captured Via CJ with BsmAI

**(Nucleotide sequence is SEQ ID NO: 481, Amino acid sequence is SEQ ID NO: 482)**

```
! 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
! S A Q D I Q M T Q S P A T L S
! aGT GCA Caa gac atc cag atg acc cag tct cca gcc acc ctg tct
! ApaLI... a gcc acc ! L25,L6,L20,L2,L16,A11
! Extender.....Bridge...

! 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
! V S P G E R A T L S C R A S Q
! gtg tct cca ggg gaa agg gcc acc ctc tcc tgc agg gcc agt cag

! 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
! S V S N N L A W Y Q Q K P G Q
! agt gtt agt aac aac tta gcc tgg tac cag cag aaa cct ggc cag

! 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
! V P R L L I Y G A S T R A T D
! gtt ccc agg ctc ctc atc tat ggt gca tcc acc agg gcc act gat

! 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75
! I P A R F S G S G S G T D F T
! atc cca gcc agg ttc agt ggc agt ggg tct ggg aca gac ttc act

! 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90
! L T I S R L E P E D F A V Y Y
! ctc acc atc agc aga ctg gag cct gaa gat ttt gca gtg tat tac

! 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105
! C Q R Y G S S P G W T F G Q G
! tgt cag cgg tat ggt agc tca ccg ggg tgg acg ttc ggc caa ggg

! 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
! T K V E I K R T V A A P S V F
! acc aag gtg gaa atc aaa cga act gtg gct gca cca tct gtc ttc

! 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135
! I F P P S D E Q L K S G T A S
! atc ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc tct

! 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150
! V V C L L N N F Y P R E A K V
! gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta

! 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165
! Q W K V D N A L Q S G N S Q E
! cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag
```

! 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180  
! S V T E Q D S K D S T Y S L S  
agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc agc

! 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195  
! S T L T L S K A D Y E K H K V  
agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc

! 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210  
! Y A C E V T H Q G L S S P V T  
tac gcc tgc gaa gtc acc cat cag ggc ctg agc tgc cct gtc aca

! 211 212 213 214 215 216 217 218 219 220 221 222 223  
! K S F N K G E C K G E F A  
aag agc ttc aac aaa gga gag tgt aag ggc gaa ttc gc.....

---

Please delete Table 26 and replace it with the following table:

Table 26: h3401-d8 KAPPA captured with CJ and *BsmAI*

**(Nucleotide sequence is SEQ ID NO: 484; Amino acid sequence is SEQ ID NO: 485)**

! 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15  
! S A Q D I Q M T Q S P A T L S  
aGTGCA Caa gac atc cag atg acc cag tct cct gcc acc ctg tct  
! ApaLI...Extender.....a gcc acc ! L25,L6,L20,L2,L16,A11  
! A GCC ACC CTG TCT ! L2 (SEQ ID NO: 483)

! 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30  
! V S P G E R A T L S C R A S Q  
gtg tct cca ggt gaa aga gcc acc ctc tcc tgc agg gcc agt cag  
! GTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC ! L2

! 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45  
! N L L S N L A W Y Q Q K P G Q  
aat ctt ctc agc aac tta gcc tgg tac cag cag aaa cct ggc cag

! 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60  
! A P R L L I Y G A S T G A I G  
gct ccc agg ctc ctc atc tat ggt gct tcc acc ggg gcc att ggt

! 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75  
! I P A R F S G S G S G T E F T  
atc cca gcc agg ttc agt ggc agt ggg tct ggg aca gag ttc act

! 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90  
! L T I S S L Q S E D F A V Y F  
ctc acc atc agc agc ctg cag tct gaa gat ttt gca gtg tat ttc

! 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105  
! C Q Q Y G T S P P T F G G G T  
tgt cag cag tat ggt acc tca ccg ccc act ttc ggc gga ggg acc

```

! 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
! K V E I K R T V A A P S V F I
  aag gtg gag atc aaa cga act gtg gct gca cca tct gtc ttc atc

! 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135
! F P P S D E Q L K S G T A S V
  ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc tct gtt

! 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150
! V C P L N N F Y P R E A K V Q
  gtg tgc ccg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag

! 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165
! W K V D N A L Q S G N S Q E S
  tgg aag gtg gat aac gcc ctc caa tgg ggt aac tcc cag gag agt

! 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180
! V T E Q D N K D S T Y S L S S
  gtc aca gag cag gac aac aag gac agc acc tac agc ctc agc agc

! 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195
! T L T L S K V D Y E K H E V Y
  acc ctg acg ctg agc aaa gta gac tac gag aaa cac gaa gtc tac

! 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210
! A C E V T H Q G L S S P V T K
  gcc tgc gaa gtc acc cat cag ggc ctt agc tgc ccc gtc acg aag

! 211 212 213 214 215 216 217 218 219 220 221 222 223
! S F N R G E C K K E F V
  agc ttc aac agg gga gag tgt aag aaa gaa ttc gtt t

```

Please delete Table 27 and replace it with the following table:

Table 27: V3-23 VH framework with variegated codons shown

**!(Nucleotide sequence is SEQ ID NO: 486; Amino acid sequence is SEQ ID NO: 487)**

```

!           17 18 19 20 21 22
!           A Q P A M A
!    5'-ctg tct gaa cG GCC cag ccG GCC atg gcc    29
!    3'-gac aga ctt gc cgg gtc ggc cgg tac cgg
!    Scab.....SfiI.....
!           NgoMI...
!           NcoI....
!
!    FR1(DP47/V3-23)-----
!    23 24 25 26 27 28 29 30
!    E V Q L L E S G
!    gaa|gtt|CAA|TTG|tta|gag|tct|ggg|    53
!    ctt|caa|gtt|aac|aat|ctc|aga|cca|
!           | MfeI |
!

```

```

! -----FR1-----
! 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
!   G G L V Q P G G S L R L S C A
! ggc|ggg|ctt|gtt|cag|cct|ggg|ggg|tct|tta|cgt|ctt|tct|tgc|gct| 98
! ccg|cca|gaa|caa|gtc|gga|cca|cca|aga|aat|gca|gaa|aga|acg|cga|
!
! Sites to be varied--->   ***   ***   ***
! -----FR1----->|...CDR1.....|---FR2-----
! 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
!   A S G F T F S S Y A M S W V R
! gct|TCC|GGA|ttc|act|ttc|tct|tCG|TAC|Gct|atg|tct|tgg|gtt|cgC| 143
! cga|agg|cct|aag|tga|aag|aga|agc|atg|cga|tac|aga|acc|caa|gcg|
!   | BspEI |           | BsiWI |           | BstXI.
!
!           Sites to be varies---> ***   *** ***
! -----FR2----->|...CDR2.....
! 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75
!   Q A P G K G L E W V S A I S G
! CAa|gct|ccT|GGt|aaa|ggg|ttg|gag|tgg|gtt|tct|gct|atc|tct|ggg| 188
! gtt|cga|gga|cca|ttt|cca|aac|ctc|acc|caa|aga|cga|tag|aga|cca|
! ...BstXI |
!
!           ***   ***
! .....CDR2.....|---FR3---
! 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90
!   S G G S T Y Y A D S V K G R F
! tct|ggg|ggc|agt|act|tac|tat|gct|gac|tcc|gtt|aaa|ggg|cgc|ttc| 233
! aga|cca|ccg|tca|tga|atg|ata|cga|ctg|agg|caa|ttt|cca|gcg|aag|
!
! -----FR3-----
! 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105
!   T I S R D N S K N T L Y L Q M
! act|atc|TCT|AGA|gac|aac|tct|aag|aat|act|ctc|tac|ttg|cag|atg| 278
! tga|tag|aga|tct|ctg|ttg|aga|ttc|tta|tga|gag|atg|aac|gtc|tac|
!   | XbaI |
!
! ---FR3----->|
! 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
!   N S L R A E D T A V Y Y C A K
! aac|agC|TTA|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat|tgc|gct|aaa| 323
! ttg|tcg|aat|tcc|cga|ctc|ctg|tga|cgt|cag|atg|ata|acg|cga|ttt|
!
!           | AfII |           | PstI |
!
! .....CDR3.....|---FR4-----
! 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135
!   D Y E G T G Y A F D I W G Q G
! gac|tat|gaa|ggg|act|ggg|tat|gct|ttc|gaC|ATA|TGg|ggg|caa|ggg| 368
! ctg|ata|ctt|cca|tga|cca|ata|cga|aag|ctg|tat|acc|cca|gtt|cca|
!           | NdeI |
!
! -----FR4----->|

```

! 136 137 138 139 140 141 142  
! T M V T V S S  
! |act|atG|GTC|ACC|gtc|tct|agt- 389  
! |tga|tac|cag|tgg|cag|aga|tca-  
! | BstEII |  
!  
! 143 144 145 146 147 148 149 150 151 152  
! A S T K G P S V F P  
! gcc tcc acc aaG GGC CcA tcg GTC TTC ccc-3' 419  
! **cgg agg tgg ttc ccg ggt agc cag aag ggg-5'**  
! Bsp120I. BbsI...(2/2)  
! ApaI....

(SFPRMET) 5'-ctg tct gaa cG GCC cag ccG-3' (**SEQ ID NO: 488**)  
(TOPFR1A) 5'-ctg tct gaa cG GCC cag ccG GCC atg gcc-  
gaa|gtt|CAA|TTG|tta|gag|tct|ggg|-  
|ggc|ggg|ctt|gtt|cag|cct|ggg|ggg|tct|tta-3' (**SEQ ID NO: 489**)  
(BOTFR1B) 3'-caa|gtc|gga|cca|cca|aga|aat|gca|gaa|aga|acg|cga|-  
|cga|agg|cct|aag|tga|aag-5' ! bottom strand (**SEQ ID NO: 490**)  
(BOTFR2) 3'-acc|caa|cgg|-  
|gtt|cga|gga|cca|ttt|cca|aac|ctc|acc|caa|aga|-5' ! bottom strand (**SEQ ID NO: 491**)  
(BOTFR3) 3'- a|cga|ctg|agg|caa|ttt|cca|gcg|aag|-  
|tga|tag|aga|tct|ctg|ttg|aga|ttc|tta|tga|gag|atg|aac|gtc|tac|-  
|ttg|tcg|aat|tcc|cga|ctc|ctg|tga-5' (**SEQ ID NO: 492**)  
(F06) 5'-gC|TTA|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat|tgc|gct|aaa|-  
|gac|tat|gaa|ggg|act|ggg|tat|gct|ttc|gaC|ATA|TGg|ggg|c-3' (**SEQ ID NO: 493**)  
(BOTFR4) 3'-cga|aag|ctg|tat|acc|cca|gtt|cca|-  
|tga|tac|cag|tgg|cag|aga|tca-  
**cgg agg tgg ttc ccg ggt agc cag aag ggg-5' ! bottom strand (SEQ ID NO: 494)**  
(BOTPRCPRIM) 3'-gg ttc ccg ggt agc cag aag ggg-5' (**SEQ ID NO: 495**)

!  
! CDR1 diversity  
!

(ON-vgC1) 5'-gct|TCC|GGA|ttc|act|tct|<1>|TAC|<1>|atg|<1>|-  
! CDR1.....6859  
! tgg|gtt|cgC|CAa|gct|ccT|GG-3' (SEQ ID NO: 496)

!  
! <1> stands for an equimolar mix of {ADEF GHIKLMNPQRSTVWY}; no C  
! (this is not a sequence)  
!

! CDR2 diversity  
!

(ON-vgC2) 5'-ggg|ttg|gag|tgg|gtt|tct|<2>|atc|<2>|<3>|-  
! CDR2.....  
! |tct|ggg|ggc|<1>|act|<1>|tat|gct|gac|tcc|gtt|aaa|gg-3' (**SEQ ID NO: 497**)  
! CDR2.....

! <1> is an equimolar mixture of {ADEF GHIKLMNPQRSTVWY}; no C  
! <2> is an equimolar mixture of {YRWVGS}; no ACDEFHIKLMNPQT  
! <3> is an equimolar mixture of {PS}; no ACDEF GHIKLMNPQRTVWY

Please delete Table 28 and replace it with the following table:

**Table 28: Stuffer used in VH (SEQ ID NO: 498)**

1 TCCGGAGCTT CAGATCTGTT TGCCCTTTTG TGGGTGGTG CAGATCGGT TACGGAGATC  
61 GACCGACTGC TTGAGCAAAA GCCACGCTTA ACTGCTGATC AGGCATGGGA TGTATTCCG  
121 CAAACCAGTC GTCAGGATCT TAACCTGAGG CTTTTTTTAC CTACTCTGCA AGCAGCGACA  
181 TCTGGTTTGA CACAGAGCGA TCCGCGTCGT CAGTTGGTAG AACATTAAAC ACGTTGGGAT  
241 GGCATCAATT TGCTTAATGA TGATGGTAAA ACCTGGCAGC AGCCAGGCTC TGCCATCCTG  
301 AACGTTTGGC TGACCAAGTAT GTTGAAGCGT ACCGTAGTGG CTGCCGTACC TATGCCATTT  
361 GATAAGTGGT ACAGCGCCAG TGGCTACGAA ACAACCCAGG ACGGCCCCAAC TGGTTCGCTG  
421 AATAAAGTG TTGGAGCAA AATTTTGTAT GAGGCGGTGC AGGAGAGCAA ATCACC AATC  
481 CCACAGGCGG TTGATCTGTT TGCTGGGAAA CCACAGCAGG AGGTTGTGTT GGCTGCGCTG  
541 GAAAGATACCT GGGAGACTCT TTCCAAACGC TATGGCAATA ATGTGAGTAA CTGAAAAACA  
601 CCTGCAATGG CCTTAACGTT CCGGGCAAAT AATTCTTTG GTGTACCGCA GGCCGCAGCG  
661 GAAGAAACGC GTCATCAGGC GGAGTATCAA AACCGTGAA CAGAAAACGA TATGATTGTT  
721 TTCTCACC AA CGACAAGCGA TCGTCTCTGTG CTTCCTGGG ATGTGGTGC ACCCGGTCAG  
781 AGTGGGTTTA TTGCTCCCGA TGGAAACAGTT GATAAGCACT ATGAAGATCA GCTGAAAATG  
841 TACGAAAATT TTGGCCGTAA GTCGCTCTG TTAACGAAAGC AGGATGTGGA GCGGCATAAG  
901 GAGTCGTCTA GA

Please delete Table 29 and replace it with the following table:

Table 29: DNA sequence of pCES5

! pCES5 6680 bases = pCes4 with stuffers in CDR1-2 and CDR3 2000.12.13

!

! Ngene = 6680

! Useful REs (cut MAnoLI fewer than 3 times) 2000.06.05

!

! Non-cutters

!Acc65I Ggtacc AfeI AGCgct AvrII Cctagg

!BsaBI GATNNnnatc BsiWI Cgtacg BsmFI Nnnnnnnnnnnnnnnngtccc

(SEQ ID NO: 499)

(SEQ ID NO: 500)

!BsrGI Tgtaca BstAPI GCANNNNntgc BstBI Ttcgaa

(SEQ ID NO: 501)

!BstZ17I GTAtac BtrI CACgtg Ecl136I GAGctc

!EcoRV GATatc FseI GGCCGGcc KpnI GGTACc

!MscI TGGcca NruI TCGoga NsiI ATGCAc

!PacI TTAATtaa PmeI GTTTaaac PmlI CACgtg

!PpuMI RGgwccy PshAI GACNNnnngtc SacI GAGCTc

(SEQ ID NO: 502)

!SacII CCGCgg SbfI CCTGCagg SexAI Accwgg

!SgfI GCGATcgc SnaBI TACgta SpeI Actagt

!SphI GCATGc Sse8387I CCTGCagg StuI AGGcct

!SwaI ATTTaaat XmaI Cccggg

!

! cutters

! Enzymes that cut more than 3 times.

!AlwNI CAGNNNctg 5

!BsgI ctgcac 4

!BsrFI Rccggy 5

!EarI CTCTTCNnnn 4

(SEQ ID NO: 625)

!FauI nNNNNNNGCGGG 10

! (SEQ ID NO: 503)

! Enzymes that cut from 1 to 3 times.

!

!EcoO109I RGgnccy 3 7 2636 4208

!BssSI Ctcgtg 1 12

!-"- Cacgag 1 1703

!BspHI Tcatga 3 43 148 1156

!AatII GACGTc 1 65

!BciVI GTATCCNNNNNNN 2 140 1667

(SEQ ID NO: 504)

!Eco57I CTGAAG 1 301

!-"- cttcag 2 1349

!AvaI Cycgrg 3 319 2347 6137

!BsiHKAII GWGCWc 3 401 2321 4245

!HgiAI GWGCWc 3 401 2321 4245

!BcgI gcannnnnnntcg 1 461

(SEQ ID NO: 505)

!ScaI AGTact	1	505
!PvuI CGATcg	3	616 3598 5926
!FspI TGCgca	2	763 5946
!BglI GCCNNNNnggc	3	864 2771 5952
<b><u>(SEQ ID NO: 506)</u></b>		
!BpmI CTGGAG	1	898
!"- ctccag	1	4413
!BsaI GGTCTCNnnnn	1	916
<b><u>(SEQ ID NO: 507)</u></b>		
!AhdI GACNNNnngtc	1	983
<b><u>(SEQ ID NO: 508)</u></b>		
!Eam1105I GACNNNnngtc	1	983
<b><u>(SEQ ID NO: 509)</u></b>		
!DrdI GACNNNnngtc	3	1768 6197 6579
<b><u>(SEQ ID NO: 510)</u></b>		
!SapI gaagagc	1	1998
!PvuII CAGctg	3	2054 3689 5896
!PfiMI CCANNNNntgg	3	2233 3943 3991
<b><u>(SEQ ID NO: 511)</u></b>		
!HindIII Aagctt	1	2235
!ApaLI Gtgcac	1	2321
!BspMI Nnnnnnnnngcaggt	1	2328
<b><u>(SEQ ID NO: 512)</u></b>		
!"- ACCTGCNNNNn	2	3460
<b><u>(SEQ ID NO: 513)</u></b>		
!PstI CTGCag	1	2335
!AccI GTmkac	2	2341 2611
!HincII GTYrac	2	2341 3730
!SalI Gtcgac	1	2341
!TliI Ctcgag	1	2347
!XhoI Ctcgag	1	2347
!BbsI gtcttc	2	2383 4219
!BlpI GCtnagc	1	2580
!EspI GCtnagc	1	2580
!SgrAI CRccggyg	1	2648
!AgeI Accggt	2	2649 4302
!AscI GGcgcgcc	1	2689
!BssHII Gcgcgcc	1	2690
!SfiI GGCCNNNNnggcc	1	2770
<b><u>(SEQ ID NO: 514)</u></b>		
!NaeI GCCggc	2	2776 6349
!NgoMIV Gccggc	2	2776 6349
!BtgI Ccrygg	3	2781 3553 5712
!DsaI Ccrygg	3	2781 3553 5712
!NcoI Ccatgg	1	2781
!StyI Ccwwgg	3	2781 4205 4472
!MfeI Caattg	1	2795
!BspEI Tccgga	1	2861
!BglII Agatct	1	2872
!BclI Tgatca	1	2956
!Bsu36I CCtnagg	3	3004 4143 4373
!XcmI CCANNNNNnnntgg	1	3215
<b><u>(SEQ ID NO: 515)</u></b>		



!MluI Acgagt 1 3527  
 !HpaI GTTaac 1 3730  
 !XbaI Tctaga 1 3767  
 !  
 !AflII Cttaag 1 3811  
 !BsmI NGcattc 1 3821  
 !"- GAATGCN 1 4695  
 !RsrII CGgwccg 1 3827  
 !NheI Gctagc 1 4166  
 !BstEII Ggtnacc 1 4182  
 !BsmBI CGTCTCNnnnn 2 4188 6625  
(SEQ ID NO: 516)  
 !"- Nnnnnngagacg 1 6673  
(SEQ ID NO: 517)  
 !ApaI GGGCCc 1 4209  
 !BanII GRGCYc 3 4209 4492 6319  
 !Bsp120I Gggccc 1 4209  
 !PspOMI Gggccc 1 4209  
 !BseRI NNnnnnnnnnctcctc 1 4226  
(SEQ ID NO: 518)  
 !"- GAGGAGNNNNNNNNNN 1 4957  
(SEQ ID NO: 519)  
 !EcoNI CCTNNnnnagg 1 4278  
(SEQ ID NO: 520)  
 !PflFI GACNnngtc 1 4308  
 !Tth111I GACNnngtc 1 4308  
 !KasI Ggcgcc 2 4327 5967  
 !BstXI CCANNNNNNntgg 1 4415  
(SEQ ID NO: 521)  
 !NotI GCggccgc 1 4507  
 !EagI Cggccg 1 4508  
 !BamHI Ggatcc 1 5169  
 !BspDI ATcgat 1 5476  
 !NdeI CATatg 1 5672  
 !EcoRI Gaattc 1 5806  
 !PsiI TTAtaa 1 6118  
 !DraIII CACNNNgtg 1 6243  
 !BsaAI YACgtr 1 6246  
 !-----

**(Nucleotide sequence is SEQ ID NO: 522 and Amino acid sequence is SEQ ID NO: 523, respectively)**

1 gacgaaaggg cCTCGTGata cgctatatt tataggttaa tgtcatgata ataattggtt  
 ! BssSI.(1/2)  
 61 cttAGACGTC aggtggcact ttctggggaa atgtgcgcgg aaccttatt tgtttattt  
 ! AatII.  
 121 tctaaatata tcaaatatG TATCCgctca tgagacaata acctgataa atgcttcaat  
 ! BciVI..(1 of 2)  
 181 aatattgaaa aaggaagagt  
 ! Base # 201 to 1061 = ApR gene from pUC119 with some RE sites removed  
 !  
 ! 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15  
 ! fM S I Q H F R V A L I P F F A  
 201 atg agt att caa cat ttc cgt gtc gcc ctt att ccc ttt ttt gcg  
 !

```

!      16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
!      A F C L P V F A H P E T L V K
246    gca ttt tgc ctt cct gtt ttt gct cac cca gaa acg ctg gtg aaa
!
!      31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
!      V K D A E D Q L G A R V G Y I
291    gta aaa gat gct gaa gat cag ttg ggt gcc cga gtg ggt tac atc
!
!      46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
!      E L D L N S G K I L E S F R P
336    gaa ctg gat ctc aac agc ggt aag atc ctt gag agt ttt cgc ccc
!
!      61 62 63 64 65 66 67 68 69 70 71 72 73 74 75
!      E E R F P M M S T F K V L L C
381    gaa gaa cgt ttt cca atg atg agc act ttt aaa gtt ctg cta tgt
!
!      76 77 78 79 80 81 82 83 84 85 86 87 88 89 90
!      G A V L S R I D A G Q E Q L G
426    ggc gcg gta tta tcc cgt att gac gcc ggg caa gaG CAa ctc ggT
!
!                               BcgI.....
!
!      91 92 93 94 95 96 97 98 99 100 101 102 103 104 105
!      R R I H Y S Q N D L V E Y S P
471    CGc cgc ata cac tat tct cag aat gac ttg gtt gAG TAC Tca cca
!..BcgI.....
!                               ScaI....
!
!      106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
!      V T E K H L T D G M T V R E L
516    gtc aca gaa aag cat ctt acg gat ggc atg aca gta aga gaa tta
!
!      121 122 123 124 125 126 127 128 129 130 131 132 133 134 135
!      C S A A I T M S D N T A A N L
561    tgc agt gct gcc ata acc atg agt gat aac act gcg gcc aac tta
!
!      136 137 138 139 140 141 142 143 144 145 146 147 148 149 150
!      L L T T I G G P K E L T A F L
606    ctt ctg aca aCG ATC Gga gga ccg aag gag cta acc gct ttt ttg
!
!                               PvuI.... (1/2)
!
!      151 152 153 154 155 156 157 158 159 160 161 162 163 164 165
!      H N M G D H V T R L D R W E P
651    cac aac atg ggg gat cat gta act cgc ctt gat cgt tgg gaa ccg
!
!      166 167 168 169 170 171 172 173 174 175 176 177 178 179 180
!      E L N E A I P N D E R D T T M
696    gag ctg aat gaa gcc ata cca aac gag gag cgt gac acc acg atg
!
!      181 182 183 184 185 186 187 188 189 190 191 192 193 194 195
!      P V A M A T T L R K L L T G E
741    cct gta GCA ATG gca aca acg tTG CGC Aaa cta tta act ggc gaa
!
!                               BsrDI..(1/2)    FspI.... (1/2)
!
!      196 197 198 199 200 201 202 203 204 205 206 207 208 209 210

```

! L L T L A S R Q Q L I D W M E  
 786 cta ctt act cta gct tcc cgg caa caa tta ata gac tgg atg gag  
 !  
 ! 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225  
 ! A D K V A G P L L R S A L P A  
 831 gcg gat aaa gtt gca gga cca ctt ctg cgc tgc gcc ctt ccg gct  
 !  
 ! 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240  
 ! G W F I A D K S G A G E R G S  
 876 ggc tgg ttt att gct gat aaa tCT GGA Gcc ggt gag cgt gGG TCT  
 ! BpmI....(1/2) BsaI....  
 !  
 ! 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255  
 ! R G I I A A L G P D G K P S R  
 921 Cgc ggt atC ATT GCa gca ctg ggg cca gat ggt aag ccc tcc cgt  
 ! BsaI..... BsrDI...(2/2)  
 !  
 ! 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270  
 ! I V V I Y T T G S Q A T M D E  
 966 atc gta gtt atc tac acG ACg ggg aGT Cag gca act atg gat gaa  
 ! AhdI.....  
 !  
 ! 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285  
 ! R N R Q I A E I G A S L I K H  
 1011 cga aat aga cag atc gct gag ata ggt gcc tca ctg att aag cat  
 !  
 ! 286 287  
 ! W .  
 1056 tgg taa  
 1062 ctgtcagac caagtttact  
 1081 catatatact ttagattgat ttaaaacttc attttaatt taaaaggatc taggtgaaga  
 1141 tcctttttga taatctcatg accaaaaatcc ctaacgtga gtttcgttc cactgagcgt  
 1201 cagaccccggt agaaaagatc aaaggatctt ctgagatcc ttttttctg cgcgtaactt  
 1261 gctgcttgca aacaaaaaaaa ccaccgctac cagcgggtggt ttgtttgccc gatcaagagc  
 1321 taccaactct ttttccgaag gtaactggct tcagcagagc gcagatacca aatactgtcc  
 1381 ttctagtgtg gccgtagtta ggccaccact tcaagaactc tgtagcaccg cctacatacc  
 1441 tcgctctgct aatcctgtta ccagtggctg ctgccagtgg cgataagtcg tgtcttaccg  
 1501 ggttgagctc aagacgatag ttaccggata agcgcagcgc gtcgggctga acgggggggt  
 1561 cgtgcataca gcccgacttg gagcgaacga cctacaccga actgagatac ctacagcgtg  
 1621 agcattgaga aagcgccacg cttcccgaag ggagaaagc ggacagGTAT CCggttaagc  
 ! BciVI.. (2 of 2)  
 1681 gcagggtcgg aacaggagag cgCACGAGgg agcttccagg gggaaacgcc tggatatctt  
 ! BssSI.(2/2)  
 1741 atagtctgt cgggtttcgc cacctctgac ttgagcgtcg attttgtga tgctcgtcag  
 1801 gggggcggag cctatggaaa aacgccagca acgcggcctt ttacgggtc ctggcctttt  
 1861 gctggccttt tgctcACATG Tctttcctg cgttatcccc tgattctgtg gataaccga  
 ! PciI..  
 1921 ttaccgcctt tgagttagct gataccgctc gccgcagccg aacgaccgag cgcagcgagt  
 1981 cagtgagcga ggaagcgGAA GAGCgccccaa taogcaaacc gcctctcccc gcgcgttggc  
 ! SapI....  
 2041 cgattcatta atgCAGCTGg cagcacaggt ttcccgactg gaaagcgggc agtgagcgcga  
 ! PvuII.(1/3)  
 2101 acgcaatTAA TGTgagttag ctcaactcatt aggcacccca ggcTTTACAc ttatgcttc

```

!      ..-35..      Plac      ..-10.
2161  cggctcgtat gttgtgtgga attgtgagcg gataacaatt tcacaCAGGA AACAGCTATG
!      M13Rev_seq_primer
2221  ACcatgatta cgCCAAGCTT TGGagccttt ttttggaga ttttcaac
!      PflMI.....
!      Hind3.
! signal::linker::CLight
!
!      1  2  3  4  5  6  7  8  9 10 11 12 13 14 15
!      fM K K L L F A I P L V V P F Y (Amino acid sequence is SEQ ID NO: 524)
2269  gtg aaa aaa tta tta ttc gca att cct tta gtt gtt cct ttc tat
!
!      Linker..... End of FR4
!      16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
!      S H S A Q V Q L Q V D L E I K
2314  tct cac aGT GCA Cag gtc caa CTG CAG GTC GAC CTC GAG atc aaa
!      ApaLI..... PstI... XhoI...
!      BspMI...
!      SalI...
!      AccI...(1/2)
!      HincII.(1/2)
!
! Vlight domains could be cloned in as ApaLI-XhoI fragments.
! VL-CL(kappa) segments can be cloned in as ApaLI-AscI fragments. <-----
!
!      Ckappa-----
!      31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
!      R G T V A A P S V F I F P P S
2359  cgt gga act gtg gct gca cca tct GTC TTC atc ttc ccg cca tct
!      BbsI...(1/2)
!
!      46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
!      D E Q L K S G T A S V V C L L
2404  gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg
!
!      61 62 63 64 65 66 67 68 69 70 71 72 73 74 75
!      N N F Y P R E A K V Q W K V D
2449  aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat
!
!      76 77 78 79 80 81 82 83 84 85 86 87 88 89 90
!      N A L Q S G N S Q E S V T E Q
2494  aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag
!
!      91 92 93 94 95 96 97 98 99 100 101 102 103 104 105
!      D S K D S T Y S L S S T L T L
2539  gac agc aag gag agc acc tac agc ctc agc agc acc ctg acG CTG
!      EspI...
!
!      106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
!      S K A D Y E K H K V Y A C E V
2584  AGC aaa gca gag tac gag aaa cac aaa GTC TAC gcc tgc gaa gtc
! ...EspI.... AccI...(2/2)
!

```

```

!      121 122 123 124 125 126 127 128 129 130 131 132 133 134 135
!      T H Q G L S S P V T K S F N R
2629   acc cat cag ggc ctg agt tcA CCG GTg aca aag agc ttc aac agg
!      AgeI....(1/2)
!
!      136 137 138 139 140
!      G E C . .
2674   gga gag tgt taa taa GG CGCGCCaatt
!      AscI.....
!      BssHII.
!
2701   ctatttcaag gagacagtca ta
!
! PelB::3-23(stuffed)::CH1::III fusion gene
!
!      1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
!      M K Y L L P T A A A G L L L L (Amino acid sequence is SEQ ID NO: 525)
2723   atg aaa tac cta ttg cct acg gca gcc gct gga ttg tta tta ctc
!
!-----
!
!      16 17 18 19 20 21 22
!      A A Q P A M A
2768   gcG GCC cag ccG GCC atg gcc
!      SfiI.....
!      NgoMIV..(1/2)
!      NcoI....
!
!      FR1(DP47/V3-23)-----
!      23 24 25 26 27 28 29 30
!      E V Q L L E S G
2789   gaa|gtt|CAA|TTG|tta|gag|tct|ggg|
!      | MfeI |
!
!-----FR1-----
!      31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
!      G G L V Q P G G S L R L S C A
2813   |ggc|ggg|ctt|gtt|cag|cct|ggg|ggg|tct|tta|cgt|ctt|tct|tgc|gct|
!
!-----FR1-----
!      46 47 48
!      A S G
2858   |gct|TCC|GGA|
!      | BspEI |
!
!      Stuffer for CDR1, FR2, and CDR2----->
!      There are no stop codons in this stuffer.
2867   gcttcAGATC Tgtttgcctt
!      BglII..
2887   tttgtggggt ggtgcagatc gcgttacgga gatcgaccga ctgcttgagc aaaagccacg
2947   cttaactgcT GATCAGgcat gggatgttat tcgcaaacc agtcgtcagg atcttaacct
!      BclI...
3007   gaggcttttt ttacctactc tgcaagcagc gacatctggt ttgacacaga gcgatccgcg

```

3067 tcgtcagttg gtagaaacat taacacgttg ggatggcatc aatttgctta atgatgatgg  
 3127 taaacctgag cagcagccag gctctgccat cctgaacgtt tggctgacca gtatgttgaa  
 3187 gcgtaccgta gtggctgccg tacctatgCC Atttgataag TGGtacagcg ccagtggcta  
 ! XcmI.....  
 3247 cgaacaacc caggacggcc caactggttc gctgaatata agtgttgag caaaaattt  
 3307 gtatgaggcg gtgcaggag acaatcacc aatccacag gcggttgatc tgttgctgg  
 3367 gaaaccacag caggaggttg tgttgctgc gctggaagat acctgggaga ctcttccaa  
 3427 acgctatggc aataatgtga gtaactggaa aacacctgca atggcctaa cgttcgggc  
 3487 aaataatttc ttggtgtac cgcaggccgc agcgaagaa ACGCGTcatc aggcggagta  
 ! MluI..  
 3547 tcaaacctg ggaacagaaa acgatgatg tgtttctca ccaacgaaa gcgatcgcc  
 3607 tgtgctgcc tgggatgtgg tcgcaccgg tcagagtggg ttattgctc ccgatggaac  
 3667 agttgataag cactatgaag atcagctgaa aatgtacgaa aatttggcc gtaagtcgt  
 ! PvuII.  
 3727 ctgGTTAACg aagcaggatg tggaggcgca taaggatcg  
 ! HpaI..  
 ! HincII(2/2)  
 ! -----FR3-----  
 ! 4 5 6 7 8 9 10 11 12 13 14 15 16  
 ! 93 94 95 96 97 98 99 100 101 102 103 104 105  
 ! S R D N S K N T L Y L Q M (Amino acid sequence is SEQ ID NO: 526)  
 3767 |TCT|AGA|gac|aac|tct|aag|aat|act|ctc|tac|ttg|cag|atg|  
 ! |XbaI|  
 !  
 ! ---FR3----->|  
 ! 17 18 19 20  
 ! 106 107 108 109  
 ! N S L s l s i r s g  
 3806 |aac|agC|TTA|AG t ctg agc att CGG TCC G  
 ! |AflII| RsrII..  
 !  
 ! q h s p nt .  
 3834 gg caa cat tct cca aac tga ccagacga cacaacggc  
 3872 ttacgctaaa tccgcgcgat gggatggtaa agaggtggcg tcttgctgg cctggactca  
 3932 tcagatgaag gccaaaaatt ggcaggagtg gacacagcag gcagcgaaac aagcactgac  
 3992 catcaactgg tactatgctg atgtaaacgg caatattggt tatgtcata ctggtgctta  
 4052 tccagatcgt caatcagcc atgatccgcg attaccggt cctggtacgg gaaaatggga  
 4112 ctggaaaggg ctattgcctt ttgaaatgaa ccctaagtg tataacccc ag  
 4164 aa GCTAGC ctgcggcttc  
 ! NheI..  
 !  
 4182 G|GTC|ACC| gtc tca agc  
 ! |BstEII|  
 !  
 ! (Amino acid sequence is SEQ ID NO: 527)  
 ! 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150  
 ! A S T K G P S V F P L A P S S  
 4198 gcc tcc acc aag ggc cca tgc gtc ttc ccc ctg gca ccc tcc tcc  
 !  
 ! 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165  
 ! K S T S G G T A A L G C L V K  
 4243 aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag

```

!
!   166 167 168 169 170 171 172 173 174 175 176 177 178 179 180
!   D Y F P E P V T V S W N S G A
4288   gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc
!
!   181 182 183 184 185 186 187 188 189 190 191 192 193 194 195
!   L T S G V H T F P A V L Q S S
4333   ctg acc agc ggc gtc cac acc ttc ccg gct gtc cta cag tcc tca
!
!   196 197 198 199 200 201 202 203 204 205 206 207 208 209 210
!   G L Y S L S S V V T V P S S S
4378   gga ctc tac tcc ctc agc agc gta gtg acc gtg ccc tcc agc agc
!
!   211 212 213 214 215 216 217 218 219 220 221 222 223 224 225
!   L G T Q T Y I C N V N H K P S
4423   ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc
!
!   226 227 228 229 230 231 232 233 234 235 236 237 238
!   N T K V D K K V E P K S C
4468   aac acc aag gtg gac aaG AAA GTT GAG CCC AAA TCT TGT
!           ON-TQHCforw.....
!
!           Poly His linker
!           139 140 141 142 143 144 145 146 147 148 149 150
!           A A A H H H H H H G A A
4507   GCG GCC GCa cat cat cat cac cat cac ggg gcc gca
!           NotI.....
!           EagI....
!
!   151 152 153 154 155 156 157 158 159 160 161 162 163 164 165
!   E Q K L I S E E D L N G A A .
4543   gaa caa aaa ctc atc tca gaa gag gat ctg aat ggg gcc gca tag
!
!   Mature III----->...
!   166 167 168 169 170 171 172 173 174 175 176 177 178 179 180
!   T V E S C L A K P H T E N S F
4588   act gtt gaa agt tgt tta gca aaa cct cat aca gaa aat tca ttt
!
!   181 182 183 184 185 186 187 188 189 190 191 192 193 194 195
!   T N V W K D D K T L D R Y A N
4633   act aac gtc tgg aaa gac gac aaa act tta gat cgt tac gct aac
!
!   196 197 198 199 200 201 202 203 204 205 206 207 208 209 210
!   Y E G C L W N A T G V V V C T
4678   tat gag ggc tgt ctg tgG AAT GCt aca ggc gtt gtg gtt tgt act
!           BsmI....
!
!   211 212 213 214 215 216 217 218 219 220 221 222 223 224 225
!   G D E T Q C Y G T W V P I G L
4723   ggt gac gaa act cag tgt tac ggt aca tgg gtt cct att ggg ctt
!
!   226 227 228 229 230 231 232 233 234 235 236 237 238 239 240
!   A I P E N E G G G S E G G G S

```

4768 gct atc cct gaa aat gag ggt ggt ggc tct gag ggt ggc ggt tct  
 !  
 ! 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255  
 ! E G G G S E G G G T K P P E Y  
 4813 gag ggt ggc ggt tct gag ggt ggc ggt act aaa cct cct gag tac  
 !  
 ! 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270  
 ! G D T P I P G Y T Y I N P L D  
 4858 ggt gat aca cct att ccg ggc tat act tat atc aac cct ctc gac  
 !  
 ! 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285  
 ! G T Y P P G T E Q N P A N P N  
 4903 ggc act tat ccg cct ggt act gag caa aac ccc gct aat cct aat  
 !  
 ! 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300  
 ! P S L E E S Q P L N T F M F Q  
 4948 cct tct ctt GAG GAG tct cag cct ctt aat act ttc atg ttt cag  
 ! BseRI..(2/2)  
 !  
 ! 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315  
 ! N N R F R N R Q G A L T V Y T  
 4993 aat aat agg ttc cga aat agg cag ggt gca tta act gtt tat acg  
 !  
 ! 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330  
 ! G T V T Q G T D P V K T Y Y Q  
 5038 ggc act gtt act caa ggc act gac ccc gtt aaa act tat tac cag  
 !  
 ! 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345  
 ! Y T P V S S K A M Y D A Y W N  
 5083 tac act cct gta tca tca aaa gcc atg tat gac gct tac tgg aac  
 !  
 ! 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360  
 ! G K F R D C A F H S G F N E D  
 5128 ggt aaa ttc aga gac tgc gct ttc cat tct ggc ttt aat gaG GAT  
 ! BamHI..  
 !  
 ! 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375  
 ! P F V C E Y Q G Q S S D L P Q  
 5173 CCa ttc gtt tgt gaa tat caa ggc caa tcg tct gAC CTG Cct caa  
 ! BamHI... BspMI...(2/2)  
 !  
 ! 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390  
 ! P P V N A G G G S G G G S G G  
 5218 cct cct gtc aat gct ggc ggc ggc tct ggt ggt ggt tct ggt ggc  
 !  
 ! 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405  
 ! G S E G G G S E G G G S E G G  
 5263 ggc tct gag ggt ggc ggc tct gag ggt ggc ggt tct gag ggt ggc  
 !  
 ! 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420  
 ! G S E G G G S G G G S G S G D  
 5308 ggc tct gag ggt ggc ggt tcc ggt ggc ggc tcc ggt tcc ggt gat  
 !



! 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435  
 ! F D Y E K M A N A N K G A M T  
 5353 ttt gat tat gaa aaa atg gca aac gct aat aag ggg gct atg acc  
 !  
 ! 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450  
 ! E N A D E N A L Q S D A K G K  
 5398 gaa aat gcc gat gaa aac gcg cta cag tct gac gct aaa ggc aaa  
 !  
 ! 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465  
 ! L D S V A T D Y G A A I D G F  
 5443 ctt gat tct gtc gct act gat tac ggt gct gct ATC GAT ggt ttc  
 ! BspDI..  
 !  
 ! 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480  
 ! I G D V S G L A N G N G A T G  
 5488 att ggt gac gtt tcc ggc ctt gct aat ggt aat ggt gct act ggt  
 !  
 ! 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495  
 ! D F A G S N S Q M A Q V G D G  
 5533 gat ttt gct ggc tct aat tcc caa atg gct caa gtc ggt gac ggt  
 !  
 ! 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510  
 ! D N S P L M N N F R Q Y L P S  
 5578 gat aat tca cct tta atg aat aat ttc cgt caa tat tta cct tct  
 !  
 ! 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525  
 ! L P Q S V E C R P Y V F G A G  
 5623 ttg cct cag tcg gtt gaa tgt cgc cct tat gtc ttt ggc gct ggt  
 !  
 ! 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540  
 ! K P Y E F S I D C D K I N L F  
 5668 aaa cCA TAT Gaa ttt tct att gat tgt gac aaa ata aac tta ttc  
 ! NdeI....  
 !  
 ! 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555  
 ! R G V F A F L L Y V A T F M Y  
 5713 cgt ggt gtc ttt gcg ttt ctt tta tat gtt gcc acc ttt atg tat  
 !  
 ! 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570  
 ! V F S T F A N I L R N K E S .  
 5758 gta ttt tcg acg ttt gct aac ata ctg cgt aat aag gag tct taa  
 !  
 ! 571  
 !  
 5803 taa GAATTC  
 ! EcoRI.  
 5812 actggccgt cgttttaca cgtcgtgact gggaaaaccc tggcggtacc caacttaac  
 5871 gccttgacg acatccccct ttcgccagct ggcgtaatag cgaagaggcc cgcacCGATC  
 ! PvuI..  
 5931 Gcccttccca acagtTGCGC Agcctgaatg gcaaatGGCG CCtgatgagg tattttctcc  
 ! ...PvuI... (3/3) FspI... (2/2) KsI...(2/2)  
 5991 ttacgatct gtgcggtatt tcacaccgca tataaattgt aaacgtaat atttgttaa

6051 aattcgcgtt aaattttgt taaatcagct catTTTTaa ccaataggcc gaaatcggca  
 6111 aaatcccTTA TAAatcaaaa gaatagcccg agatagggtt gagtgtgtt ccagtttgga  
 ! PsiI...  
 6171 acaagagtcc actattaaag aacgtggact ccaacgtcaa agggcgaaaa accgtctatc  
 6231 agggcgatgg ccCACtacGT Gaaccatcac ccaaataag tttttgggg tcgaggtgcc  
 ! DraIII....  
 6291 gtaaagcact aaatcggaac cctaaaggga gcccccgatt tagagcttga cggggaaaGC  
 ! NgoMIV..  
 6351 CGGCgaacgt ggcgagaaaag gaagggaaga aagcgaaagg agcgggcgct agggcgctgg  
 ! ..NgoMIV.(2/2)  
 6411 caagtgtagc ggtcacgctg cgcgtaacca ccacaccgc cgcgcttaat gcgcgctac  
 6471 agggcgcgta ctatggttgc ttgacgggt gcagtctcag tacaatctgc tctgatgccg  
 6531 catagttaag ccagccccga caccgcca caccgctga cgcgcctga cgggcttgc  
 6591 tgctccggc atccgcttac agacaagctg tgaccgtctc cgggagctgc atgtgtcaga  
 6651 ggtttcacc gtcacaccg aaacgcgca

Please delete Table 30 and replace it with the following table:

Table 30: Oligonucleotides used to clone CDR1/2 diversity

All sequences are 5' to 3'.

1) ON\_CD1Bsp, 30 bases **(SEQ ID NO: 528)**

A c c T c A c T g g c T T c c g g A  
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18

T T c A c T T T c T c T  
19 20 21 22 23 24 25 26 27 28 29 30

2) ON\_Br12, 42 bases **(SEQ ID NO: 529)**

A g A A A c c c A c T c c A A A c c  
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18

T T T A c c A g g A g c T T g g c g  
19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36

A A c c c A  
37 38 39 40 41 42

3) ON\_CD2Xba, 51 bases **(SEQ ID NO: 530)**

g g A A g g c A g T g A T c T A g A  
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18

g A T A g T g A A g c g A c c T T T  
19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36

A A c g g A g T c A g c A T A  
37 38 39 40 41 42 43 44 45 46 47 48 49 50 51

4) ON\_BotXba, 23 bases **(SEQ ID NO: 531)**

g g A A g g c A g T g A T c T A g A  
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18

g A T A g  
19 20 21 22 23

Please delete Table 31 and replace it with the following table:

Table 31: Bridge/Extender Oligonucleotides

**(SEQ ID NOS 532-546, respectively in order of appearance)**

ON_Lam1aB7(rc)	.....GTGCTGACTCAGCCACCCTC.	20
ON_Lam2aB7(rc)	.....GCCCTGACTCAGCCTGCCTC.	20
ON_Lam31B7(rc)	.....GAGCTGACTCAGG.ACCCTGC	20
ON_Lam3rB7(rc)	.....GAGCTGACTCAGCCACCCTC.	20
ON_LamHf1cBrg(rc)	CCTCGACAGCGAAGTGCACAGAGCGTCTTGACTCAGCC.....	38
ON_LamHf1cExt	CCTCGACAGCGAAGTGCACAGAGCGTCTTG.....	30
ON_LamHf2b2Brg(rc)	CCTCGACAGCGAAGTGCACAGAGCGCTTTGACTCAGCC.....	38
ON_LamHf2b2Ext	CCTCGACAGCGAAGTGCACAGAGCGCTTTG.....	30
ON_LamHf2dBrg(rc)	CCTCGACAGCTAAGTGCACAGAGCGCTTTGACTCAGCC.....	38
ON_LamHf2dExt	CCTCGACAGCGAAGTGCACAGAGCGCTTTG.....	30
ON_LamHf31Brg(rc)	CCTCGACAGCGAAGTGCACAGAGCGAATTGACTCAGCC.....	38
ON_LamHf31Ext	CCTCGACAGCGAAGTGCACAGAGCGAATTG.....	30
ON_LamHf3rBrg(rc)	CCTCGACAGCGAAGTGCACAGTACGAATTGACTCAGCC.....	38
ON_LamHf3rExt	CCTCGACAGCGAAGTGCACAGTACGAATTG.....	30
ON_lamPlePCR	CCTCGACAGCGAAGTGCACAG.....	21
Consensus		

Please delete Table 32 and replace it with the following table:

Table 32: Oligonucleotides used to make SSDNA locally double-stranded

**(SEQ ID NOS 548-552, respectively in order of appearance)**

Adapters (8)

H43HF3.1?02#1	5'-cc gtg tat tac tgt gcg aga g-3'
H43.77.97.1-03#2	5'-ct gtg tat tac tgt gcg aga g-3'
H43.77.97.323#22	5'-cc gta tat tac tgt gcg aaa g-3'
H43.77.97.330#23	5'-ct gtg tat tac tgt gcg aaa g-3'
H43.77.97.439#44	5'-ct gtg tat tac tgt gcg aga c-3'
H43.77.97.551#48	5'-cc atg tat tac tgt gcg aga c-3'

Please delete Table 33 and replace it with the following table:

Table 33: Bridge/extender pairs

Bridges (2)

H43.XABr1

5'ggtgtagtgaTCTAGtgacaactctaagaatactctctacttgcagatgaacagCTTtAGggc  
tgaggacaCTGCAGtctactattgtgcgaga-3' **(SEQ ID NO: 553)**

H43.XABr2

5'ggtgtagtgaTCTAGtgacaactctaagaatactctctacttgcagatgaacagCTTtAGggc  
tgaggacaCTGCAGtctactattgtgcgaaa-3' **(SEQ ID NO: 554)**

Extender

H43.XAExt

5'ATAgTAgAcTgcAgTgTccTcAgcccTTAAGcTgTTcATcTgcAAgTAgAgAgTATTcTTAg  
gTTgTcTcTAgATcAcTAcAcc-3'. **(SEQ ID NO: 555)**

Please delete Table 34 and replace it with the following table:

## Primers

Please delete Table 36 and replace it with the following table:

!BspDI ATcgat	2	2520	9883	
!NdeI CATatg	3	2716	3796	9847
!End gene III		2846		
!Start gene VI		2848		
!AfeI AGCgct	1	3032		
!End gene VI		3187		
!Start gene I		3189		
!EarI CTCTTCNnnn	2	4067	9274	
<u>(SEQ ID NO: 563)</u>				
!-"- Nnnnngaagag	2	6126	8953	
<u>(SEQ ID NO: 564)</u>				
!PacI TTAATtaa	1	4125		
!Start gene IV		4213		
!End gene I		4235		
!BsmFI Nnnnnnnnnnnnnnnngtccc	2	5068	9515	
<u>(SEQ ID NO: 565)</u>				
!MscI TGGcca	3	5073	7597	9160
!PsiI TTAtaa	2	5349	5837	
!End gene IV		5493		
!Start ori		5494		
!NgoMIV Gccggc	3	5606	8213	9315
!BanII GRGCYc	4	5636	8080	8606 8889
!DraIII CACNNNgtg	1	5709		
!DrdI GACNNNNnngtc	1	5752		
<u>(SEQ ID NO: 566)</u>				
!AvaI Cycgrg	2	5818	7240	
!PvuII CAGctg	1	5953		
!BsmBI CGTCTCNnnnn	3	5964	8585	9271
<u>(SEQ ID NO: 567)</u>				
!End ori region		5993		
!BamHI Ggatcc	1	5994		
!HindIII Aagctt	3	6000	7147	7384
!BciVI GTATCCNNNNNN	1	6077		
<u>(SEQ ID NO: 568)</u>				
!Start bla		6138		
!Eco57I CTGAAG	2	6238	7716	
!SpeI Actagt	1	6257		
!BcgI gcannnnnntcg	1	6398		
<u>(SEQ ID NO: 569)</u>				
!ScaI AGTact	1	6442		
!PvuI CGATcg	1	6553		
!FspI TGCgca	1	6700		
!BglI GCCNNNNnggc	3	6801	8208	8976
<u>(SEQ ID NO: 570)</u>				
!BsaI GGTCTCNnnnn	1	6853		
<u>(SEQ ID NO: 571)</u>				
!AhdI GACNNNNnngtc	1	6920		
<u>(SEQ ID NO: 572)</u>				
!Eam1105I GACNNNNnngtc	1	6920		
<u>(SEQ ID NO: 573)</u>				
!End bla		6998		
!AccI GTmkac	2	7153	8048	
!HincII GTYrac	1	7153		
!SalI Gtcgac	1	7153		
!XhoI Ctcgag	1	7240		
!Start PlacZ region		7246		
!End PlacZ region		7381		
!PflMI CCANNNNntgg	1	7382		

```

      (SEQ ID NO: 574)
!RBS1                                7405
!start M13-iii signal seq for LC    7418
!ApaLI Gtgcac                        1 7470
!end M13-iii signal seq              7471
!Start light chain kappa L20:JK1     7472
!PflFI GACNnngtc                    3 7489 8705 9099
!SbfI CCTGCAGg                      1 7542
!PstI CTGCAG                        1 7543
!KpnI GGTACc                        1 7581
!XcmI CCANNNNNnnnntgg               2 7585 9215
      (SEQ ID NO: 575)
!NsiI ATGCAt                        2 7626 9503
!BsgI ctgcac                        1 7809
!BbsI gtcttc                        2 7820 8616
!BlpI GCTnagc                       1 8017
!EspI GCTnagc                       1 8017
!EcoO109I RGgnccy                   2 8073 8605
!Ecl136I GAGctc                     1 8080
!SacI GAGCTc                        1 8080
!End light chain                     8122
!AscI GGcgcgcc                      1 8126
!BssHII Gcgcgcc                     1 8127
!RBS2                                8147
!SfiI GGCCNNNNnggcc                 1 8207
      (SEQ ID NO: 576)
!NcoI Ccatgg                        1 8218
!Start 3-23, FR1                     8226
!MfeI Caattg                        1 8232
!BspEI Tccgga                       1 8298
!Start CDR1                          8316
!Statt FR2                          8331
!BstXI CCANNNNNntgg                 2 8339 8812
      (SEQ ID NO: 577)
!EcoNI CCTNNnnnagg                  2 8346 8675
      (SEQ ID NO: 578)
!Start FR3                           8373
!XbaI Tctaga                        2 8436 1643
!AflII Cttaag                       1 8480
!Start CDR3                          8520
!AatII GACGTc                       1 8556
!Start FR4                          8562
!PshAI GACNNnngtc                   2 8573 9231
      (SEQ ID NO: 579)
!BstEII Ggtnacc                     1 8579
!Start CH1                          8595
!ApaI GGGCCc                        1 8606
!Bsp120I Gggccc                     1 8606
!PspOMI Gggccc                       1 8606
!AgeI Accggt                         1 8699
!Bsu36I CCtnagg                      2 8770 9509
!End of CH1                          8903
!NotI GCggccgc                      1 8904
!Start His6 tag                      8913
      (SEQ ID NO: 12)
!Start cMyc tag                      8931
!Amber codon                         8982
!NheI Gctagc                        1 8985

```

```

!Start M13 III Domain 3      8997
!NruI TCGcga                1    9106
!BstBI TTcgaa               1    9197
!EcoRI Gaattc                1    9200
!XcmI CCANNNNNnnnntgg      1    9215
  (SEQ ID NO: 580)
!BstAPI GCANNNNntgc        1    9337
  (SEQ ID NO: 581)
!SacII CCGCgg              1    9365
!End IIIstump anchor        9455
!AvrII Cctagg              1    9462
!trp terminator             9470
!SwaI ATTTaaat             1    9784
!Start gene II              9850
!BglII Agatct              1    9936

```

-----  
 (SEQ ID NO: 582)

```

      1 aat gct act act att agt aga att gat gcc acc ttt tca gct cgc gcc
! gene ii continued
      49 cca aat gaa aat ata gct aaa cag gtt att gac cat ttg cga aat gta
      97 tct aat ggt caa act aaa tct act cgt tcg cag aat tgg gaa tca act
     145 gtt aTa tgg aat gaa act tcc aga cac cgt act tta gtt gca tat tta
     193 aaa cat gtt gag cta cag caT TaT att cag caa tta agc tct aag cca
     241 tcc gca aaa atg acc tct tat caa aag gag caa tta aag gta ctc tct
     289 aat cct gac ctg ttg gag ttt gct tcc ggt ctg gtt cgc ttt gaa gct
     337 cga att aaa acg cga tat ttg aag tct ttc ggg ctt cct ctt aat ctt
     385 ttt gat gca atc cgc ttt gct tct gac tat aat agt cag ggt aaa gac
     433 ctg att ttt gat tta tgg tca ttc tcg ttt tct gaa ctg ttt aaa gca
     481 ttt gag ggg gat tca ATG aat att tat gac gat tcc gca gta ttg gac
! Start gene x, ii continues
     529 gct atc cag tct aaa cat ttt act att acc ccc tct ggc aaa act tct
     577 ttt gca aaa gcc tct cgc tat ttt ggt ttt tat cgt cgt ctg gta aac
     625 gag ggt tat gat agt gtt gct ctt act atg cct cgt aat tcc ttt tgg
     673 cgt tat gta tct gca tta gtt gaa tgt ggt att cct aaa tct caa ctg
     721 atg aat ctt tct acc tgt aat aat gtt gtt ccg tta gtt cgt ttt att
     769 aac gta gat ttt tct tcc caa cgt cct gac tgg tat aat gag cca gtt
     817 ctt aaa atc gca TAA
! End X & II
     832 ggtaattca ca

```

! (SEQ ID NO: 626)

```

! M1 E5 Q10 T15
  843 ATG att aaa gtt gaa att aaa cca tct caa gcc caa ttt act act cgt
! Start gene V
!
! S17 S20 P25 E30
  891 tct ggt gtt tct cgt cag ggc aag cct tat tca ctg aat gag cag ctt
!
! V35 E40 V45
  939 tgt tac gtt gat ttg ggt aat gaa tat ccg gtt ctt gtc aag att act
!
! D50 A55 L60
  987 ctt gat gaa ggt cag cca gcc tat gcg cct ggt cTGATAC Acc gtt cat
! BsrGI...
! L65 V70 S75 R80
 1035 ctg tcc tct ttc aaa gtt ggt cag ttc ggt tcc ctt atg att gac cgt
!
! P85 K87 end of V

```



```

1083 ctg cgc ctc gtt ccg gct aag TAA C
!
1108 ATG gag cag gtc gcg gat ttc gac aca att tat cag gcg atg
!   Start gene VII
!
1150 ata caa atc tcc gtt gta ctt tgt ttc gcg ctt ggt ata atc
!
!               VII and IX overlap.
!               ..... S2  V3  L4  V5 (SEQ ID NO: 621) S10
1192 gct ggg ggt caa agA TGA gt gtt tta gtg tat tct ttt gcc tct ttc
gtt
!               End VII
!               |start IX
!           L13       W15               G20               T25
E29
1242 tta ggt tgg tgc ctt cgt agt ggc att acg tat ttt acc cgt tta atg
gaa
!
1293 act tcc tc
!
!   .... stop of IX, IX and VIII overlap by four bases
1301 ATG aaa aag tct tta gtc ctc aaa gcc tct gta gcc gtt gct acc ctc
!   Start signal sequence of viii.
!
1349 gtt ccg atg ctg tct ttc gct gct gag ggt gac gat ccc gca aaa gcg
!               mature VIII --->
1397 gcc ttt aac tcc ctg caa gcc tca gcg acc gaa tat atc ggt tat gcg
1445 tgg gcg atg gtt gtt gtc att
1466 gtc ggc gca act atc ggt atc aag ctg ttt aag
!
! bases 1499-1539 are probable promoter for iii
1499 aaa ttc acc tcg aaa gca ! 1515
!   ..... -35 ..
!
1517      agc tga taaaccgat acaattaaag gctccttttg
!               ..... -10   ...
!
1552 gagccttttt ttt GGAGAt ttt ! S.D. uppercase, there may be 9 Ts
!
!   <----- III signal sequence ----->
(SEQ ID NO: 583)
!           M   K   K   L   L   F   A   I   P   L   V   V   P   F
1574 caac GTG aaa aaa tta tta ttc gca att cct tta gtt gtt cct ttc !
1620
!
!           Y   S   G   A   A   E   S   H   L   D   G   A
1620 tat tct ggc gCG GCC Gaa tca caT CTA GAc ggc gcc
!               EagI....       XbaI....
!
! Domain 1 -----
!           A   E   T   V   E   S   C   L   A
1656      gct gaa act gtt gaa agt tgt tta gca
!
!           K   S   H   T   E   I   S   F   T   N   V   W   K   D   D   K
T
1683 aaA Tcc cat aca gaa aat tca ttt aCT AAC GTC TGG AAA GAC GAC AAA
ACt
!

```

```

!       L   D   R   Y   A   N   Y   E   G   S   L   W   N   A   T   G
V
1734 tta gat cgt tac gct aac tat gag ggC tgt ctg tgG AAT GcT aca ggc
gtt
!
!                                     BsmI....
!
!       V   V   C   T   G   D   E   T   Q   C   Y   G   T   W   V   P
I
1785 gta gtt tgt act ggt GAC GAA ACT CAG TGT TAC GGT ACA TGG GTT cct
att
!
!       G   L   A   I   P   E   N
1836 ggg ctt gct atc cct gaa aat
!
! L1 linker -----
!       E   G   G   G   S   E   G   G   G   S
1857 gag ggt ggt ggc tct gag ggt ggc ggt tct
!
!       E   G   G   G   S   E   G   G   G   T
1887 gag ggt ggc ggt tct gag ggt ggc ggt act
!
! Domain 2 -----
1917 aaa cct cct gag tac ggt gat aca cct att ccg ggc tat act tat atc
aac
1968 cct ctc gac ggc act tat ccg cct ggt act gag caa aac ccc gct aat
cct
2019 aat cct tct ctt GAG GAG tct cag cct ctt aat act ttc atg ttt cag
aat
!
!                                     BseRI..
2070 aat agg ttc cga aat agg cag ggg gca tta act gtt tat acg ggc act
2118 gtt act caa ggc act gac ccc gtt aaa act tat tac cag tac act cct
2166 gta tca tca aaa gcc atg tat gac gct tac tgg aac ggt aaa ttC AGA
!
!                                     AlwNI
2214 GAC TGc gct ttc cat tct ggc ttt aat gaG gat TTa ttT gtt tgt gaa
!
!       AlwNI
2262 tat caa ggc caa tcg tct gac ctg cct caa cct cct gtc aat gct
!
2307 ggc ggc ggc tct
! start L2
-----
2319 ggt ggt ggt tct
2331 ggt ggc ggc tct
2343 gag ggt ggt ggc tct gag gga ggc ggt tcc
2373 ggt ggt ggc tct ggt ! end L2
!
! Many published sequences of M13-derived phage have a longer linker
! than shown here by repeats of the EGGGS (SEQ ID NO: 589) motif two
! more times.
!
! Domain 3
! (SEQ ID NO: 584)
-----
!       S   G   D   F   D   Y   E   K   M   A   N   A   N   K   G   A
2388 tcc ggt gat ttt gat tat gaa aag atg gca aac gct aat aag ggg gct
!
!       M   T   E   N   A   D   E   N   A   L   Q   S   D   A   K   G
2436 atg acc gaa aat gcc gat gaa aac gcg cta cag tct gac gct aaa ggc
!

```

```

!      K   L   D   S   V   A   T   D   Y   G   A   A   M   D   G   F
2484 aaa ctt gat tct gtc gct act gat tac ggt gct gct atc gat ggt ttc
!
!      I   G   D   V   S   G   L   A   N   G   N   G   A   T   G   D
2532 att ggt gac gtt tcc ggc ctt gct aat ggt aat ggt gct act ggt gat
!
!      F   A   G   S   N   S   Q   M   A   Q   V   G   D   G   D   N
2580 ttt gct ggc tct aat tcc caa atg gct caa gtc ggt gac ggt gat aat
!
!      S   P   L   M   N   N   F   R   Q   Y   L   P   S   L   P   Q
2628 tca cct tta atg aat aat ttc cgt caa tat tta cct tcc ctc cct caa
!
!      S   V   E   C   R   P   F   V   F   G   A   G   K   P   Y   E
2676 tcg gtt gaa tgt cgc cct ttt gtc ttt Ggc gct ggt aaa cca tat gaa
!
!      F   S   I   D   C   D   K   I   N   L   F   R
2724 ttt tct att gat tgt gac aaa ata aac tta ttc cgt
!                                     End Domain 3
!
!      G   V   F   A   F   L   L   Y   V   A   T   F   M   Y   V   F140
2760 ggt gtc ttt gcg ttt ctt tta tat gtt gcc acc ttt atg tat gta ttt
!      start transmembrane segment
!
!      S   T   F   A   N   I   L
2808 tct acg ttt gct aac ata ctg
!
!      R   N   K   E   S
2829 cgt aat aag gag tct TAA ! stop of iii
!      Intracellular anchor.
!      (SEQ ID NO: 585)
!      M1 P2 V L L5 G I P L L10 L R F L G15
2847 tc ATG cca gtt ctt ttg ggt att ccg tta tta ttg cgt ttc ctc ggt
!      Start VI
!
2894 ttc ctt ctg gta act ttg ttc ggc tat ctg ctt act ttt ctt aaa aag
2942 ggc ttc ggt aag ata gct att gct att tca ttg ttt ctt gct ctt att
2990 att ggg ctt aac tca att ctt gtg ggt tat ctc tct gat att agc gct
3038 caa tta ccc tct gac ttt gtt cag ggt gtt cag tta att ctc ccg tct
3086 aat gcg ctt ccc tgt ttt tat gtt att ctc tct gta aag gct gct att
3134 ttc att ttt gac gtt aaa caa aaa atc gtt tct tat ttg gat tgg gat
!
!      M1 A2 V3 F5 L10 G13
3182 aaa TAA t ATG gct gtt tat ttt gta act ggc aaa tta ggc tct gga
!      end VI Start gene I
!
! (SEQ ID NO: 586)
!      K   T   L   V   S   V   G   K   I   Q   D   K   I   V   A
3228 aag acg ctc gtt agc gtt ggt aag att cag gat aaa att gta gct
!
!      G   C   K   I   A   T   N   L   D   L   R   L   Q   N   L
3273 ggg tgc aaa ata gca act aat ctt gat tta agg ctt caa aac ctc
!
!      P   Q   V   G   R   F   A   K   T   P   R   V   L   R   I
3318 ccg caa gtc ggg agg ttc gct aaa acg cct cgc gtt ctt aga ata
!
!      P   D   K   P   S   I   S   D   L   L   A   I   G   R   G
3363 ccg gat aag cct tct ata tct gat ttg ctt gct att ggg cgc ggt
!

```

```

!      N   D   S   Y   D   E   N   K   N   G   L   L   V   L   D
3408 aat gat tcc tac gat gaa aat aaa aac ggc ttg ctt gtt ctc gat
!
!      E   C   G   T   W   F   N   T   R   S   W   N   D   K   E
3453 gag tgc ggt act tgg ttt aat acc cgt tct tgg aat gat aag gaa
!
!      R   Q   P   I   I   D   W   F   L   H   A   R   K   L   G
3498 aga cag ccg att att gat tgg ttt cta cat gct cgt aaa tta gga
!
!      W   D   I   I   F   L   V   Q   D   L   S   I   V   D   K
3543 tgg gat att att ttt ctt gtt cag gac tta tct att gtt gat aaa
!
!      Q   A   R   S   A   L   A   E   H   V   V   Y   C   R   R
3588 cag gcg cgt tct gca tta gct gaa cat gtt gtt tat tgt cgt cgt
!
!      L   D   R   I   T   L   P   F   V   G   T   L   Y   S   L
3633 ctg gac aga att act tta cct ttt gtc ggt act tta tat tct ctt
!
!      I   T   G   S   K   M   P   L   P   K   L   H   V   G   V
3678 att act ggc tcg aaa atg cct ctg cct aaa tta cat gtt ggc gtt
!
!      V   K   Y   G   D   S   Q   L   S   P   T   V   E   R   W
3723 gtt aaa tat ggc gat tct caa tta agc cct act gtt gag cgt tgg
!
!      L   Y   T   G   K   N   L   Y   N   A   Y   D   T   K   Q
3768 ctt tat act ggt aag aat ttg tat aac gca tat gat act aaa cag
!
!      A   F   S   S   N   Y   D   S   G   V   Y   S   Y   L   T
3813 gct ttt tct agt aat tat gat tcc ggt gtt tat tct tat tta acg
!
!      P   Y   L   S   H   G   R   Y   F   K   P   L   N   L   G
3858 cct tat tta tca cac ggt cgg tat ttc aaa cca tta aat tta ggt
!
!      Q   K   M   K   L   T   K   I   Y   L   K   K   F   S   R
3903 cag aag atg aaa tta act aaa ata tat ttg aaa aag ttt tct cgc
!
!      V   L   C   L   A   I   G   F   A   S   A   F   T   Y   S
3948 gtt ctt tgt ctt gcg att gga ttt gca tca gca ttt aca tat agt
!
!      Y   I   T   Q   P   K   P   E   V   K   K   V   V   S   Q
3993 tat ata acc caa cct aag ccg gag gtt aaa aag gta gtc tct cag
!
!      T   Y   D   F   D   K   F   T   I   D   S   S   Q   R   L
4038 acc tat gat ttt gat aaa ttc act att gac tct tct cag cgt ctt
!
!      N   L   S   Y   R   Y   V   F   K   D   S   K   G   K   L
4083 aat cta agc tat cgc tat gtt ttc aag gat tct aag gga aaa TTA
!
!
!
!
!      I   N   S   D   D   L   Q   K   Q   G   Y   S   L   T   Y
4128 ATT AAt agc gac gat tta cag aag caa ggt tat tca ctc aca tat
!
!      PacI
!
!      i   I   D   L   C   T   V   S   I   K   K   G   N   S   N   E
!      iv
!      4173 att gat tta tgt act gtt tcc att aaa aaa ggt aat tca aAT Gaa
!
!
!      Start IV
! (SEQ ID NO: 527)

```

```

!      i      I      V      K      C      N      .End of I
!      iv     L3     L      N5     V      I7     N      F      V10
4218      att gtt aaa tgt aat TAA T TTT GTT
! IV continued.....
4243 ttc ttg atg ttt gtt tca tca tct tct ttt gct cag gta att gaa atg
4291 aat aat tcg cct ctg cgc gat ttt gta act tgg tat tca aag caa tca
4339 ggc gaa tcc gtt att gtt tct ccc gat gta aaa ggt act gtt act gta
4387 tat tca tct gac gtt aaa cct gaa aat cta cgc aat ttc ttt att tct
4435 gtt tta cgt gcA aat aat ttt gat atg gtA ggt tcT aAC cct tcc atT
4483 att cag aag tat aat cca aac aat cag gat tat att gat gaa ttg cca
4531 tca tct gat aat cag gaa tat gat gat aat tcc gct cct tct ggt ggt
4579 ttc ttt gtt ccg caa aat gat aat gtt act caa act ttt aaa att aat
4627 aac gtt cgg gca aag gat tta ata cga gtt gtc gaa ttg ttt gta aag
4675 tct aat act tct aaa tcc tca aat gta tta tct att gac ggc tct aat
4723 cta tta gtt gtt agt gcT cct aaa gat att tta gat aac ctt cct caa
4771 ttc ctt tcA act gtt gat ttg cca act gac cag ata ttg att gag ggt
4819 ttg ata ttt gag gtt cag caa ggt gat gct tta gat ttt tca ttt gct
4867 gct ggc tct cag cgt ggc act gtt gca ggc ggt gtt aat act gac cgc
4915 ctc acc tct gtt tta tct tct gct ggt ggt tcg ttc ggt att ttt aat
4963 ggc gat gtt tta ggg cta tca gtt cgc gca tta aag act aat agc cat
5011 tca aaa ata ttg tct gtg cca cgt att ctt acg ctt tca ggt cag aag
5059 ggt tct atc tct gtT GGC CAG aat gtc cct ttt att act ggt cgt gtg
!      MscI....
5107 act ggt gaa tct gcc aat gta aat aat cca ttt cag acg att gag cgt
5155 caa aat gta ggt att tcc atg agc gtt ttt cct gtt gca atg gct ggc
5203 ggt aat att gtt ctg gat att acc agc aag gcc gat agt ttg agt tct
5251 tct act cag gca agt gat gtt att act aat caa aga agt att gct aca
5299 acg gtt aat ttg cgt gat gga cag act ctt tta ctc ggt ggc ctc act
5347 gat tat aaa aac act tct caG gat tct ggc gta ccg ttc ctg tct aaa
5395 atc cct tta atc ggc ctc ctg ttt agc tcc cgc tct gat tcT aac gag
5443 gaa agc acg tta tac gtg ctc gtc aaa gca acc ata gta cgc gcc ctg
5491 TAG cggcgcat
!      End IV
5503 aagcgcggcg ggtgtggtgg ttacgcgcag cgtgaccgct acacttgcca
gcgcctagc
5563 gcccgctcct ttcgctttct tcccttcctt tctcgccacg ttcGCCGGCT
ttccccgtca
!      NgoMI.
5623 agctctaaat cgggggctcc ctttaggggtt ccgatttagt gctttacggc
acctcgacc
5683 caaaaaactt gatttggtg atgggtCACG TAGTGggcca tcgcctgat
agacggtttt
!      DraIII....
5743 tcgccctttG ACGTTGGAGT Ccagttctt taatagtgga ctcttggtcc
aaactggaac
!      DrdI.....
5803 aacactcaac cctatctcgg gctattcttt tgatttataa gggattttgc
cgatttcgga
5863 accaccatca aacaggattt tcgcctgctg gggcaaacca gcgtggaccg
cttgctgcaa
5923 ctctctcagg gccaggcggg gaagggaat CAGCTGttgc cCGTCTCact
ggtgaaaaga
!      PvuII.      BsmBI.
5983 aaaaccaccc tGGATCC AAGCTT
!      BamHI      HindIII (1/2)
!      Insert carrying bla gene
6006      gcagggtg gcacttttcg gggaaatgtg gcgcggaaccc

```

```

6043 ctatttgttt atttttctaa atacattcaa atatGTATCC gctcatgaga
caataaccct
!
!                               BciVI
6103 gataaatgct tcaataatat tgaaaaAGGA AGAgT
!                               RBS.?...
!
!   Start bla gene
6138 ATG agt att caa cat ttc cgt gtc gcc ctt att ccc ttt ttt gcg gca
ttt
6189 tgc ctt cct gtt ttt gct cac cca gaa acg ctg gtg aaa gta aaa gat
gct
6240 gaa gat cag ttg ggC gcA CTA GTg ggt tac atc gaa ctg gat ctc aac
agc
!                               SpeI....
!                               ApaLI & BssSI Removed
6291 ggt aag atc ctt gag agt ttt cgc ccc gaa gaa cgt ttt cca atg atg
agc
6342 act ttt aaa gtt ctg cta tgt GGC GcG Gta tta tcc cgt att gac gcc
ggg
6393 caa gaG CAA CTC GGT CGc cgC ATA cAC tat tct cag aat gac ttg gtt
gAG
!                               BcgI.....
ScaI
6444 TAC Tca cca gtc aca gaa aag cat ctt acg gat ggc atg aca gta aga
gaa
!                               ScaI.
6495 tta tgc agt gct gcc ata acc atg agt gat aac act gcg gcc aac tta
ctt
6546 ctg aca aCG ATC Gga gga ccg aag gag cta acc gct ttt ttg cac aac
atg
!                               PvuI....
6597 ggg gat cat gta act cgc ctt gat cgt tgg gaa ccg gag ctg aat gaa
gcc
6648 ata cca aac gac gag cgt gac acc acg atg cct gta gca atg Gca aca
acg
6699 tTG CGC Aaa cta tta act ggc gaa cta ctt act cta gct tcc cgg caa
caa
!                               FspI....
!
6750 tta ata gac tgg atg gag gcg gat aaa gtt gca gga cca ctt ctg cgc
tcg
6801 GCC ctt ccG GcT ggc tgg ttt att gct gat aaa tct gga gcc ggt gag
cgt
!                               BglI.....
6852 gGG TCT Cgc ggt atc att gca gca ctg ggg cca gat ggt aag ccc tcc
cgt
!                               BsaI....
6903 atc gta gtt atc tac acG ACg ggg aGT Cag gca act atg gat gaa cga
aat
!                               AhdI.....
6954 aga cag atc gct gag ata ggt gcc tca ctg att aag cat tgg TAA ctgt
!                               stop
7003 cagaccaagt ttactcatat atactttaga ttgatttaaa acttcatttt
taattttaaaa
7063 ggatctaggt gaagatcctt tttgataatc tcatgaccaa aatcccttaa
cgtgagtttt
7123 cgttccactg tacgtaagac cccc
7147 AAGCTT   GTCGAC tgaa tggcgaatgg cgctttgcct
!                               HindIII   SalI..

```

```

!      (2/2)      HincII
7183 ggtttccggc accagaagcg gtgccgga gctggctgga gtgcgatctt
!
! Start of Fab-display cassette, the Fab DSR-A05, selected for
! binding to a protein antigen.
!
7233 CCTGAcG CTCGAG
!      xBsu36I XhoI..
!
! PlacZ promoter is in the following block
!
7246                                cgcaacgc aattaatgtg agttagctca
7274 ctcattaggc accccaggct ttacacttta tgcttccggc tcgtatgttg
7324 tgtggaattg tgagcggata acaatttcac acaggaaaca gctatgacca
7374 tgattacgCC AagcttTGGA gccttttttt tggagatttt caac
!
!      PflMI.....
!      Hind3. (there are 3)
! Gene iii signal sequence: (Amino acid sequence is SEQ ID NO: 587)
!      1   2   3   4   5   6   7   8   9  10  11  12  13  14  15
!      M   K   K   L   L   F   A   I   P   L   V   V   P   F   Y
7418  gtg aaa aaa tta tta ttc gca att cct tta gtt gtt cct ttc tat
!
!      16  17  18      Start light chain (L20:JK1)
!      S   H   S   A   Q   D   I   Q   M   T   Q   S   P   A
7463  tct cac aGT GCA Caa gac atc cag atg acc cag tct cca gcc
!
!      ApaLI...
!      Sequence supplied by extender.....
!
!      T   L   S   L
7505  acc ctg tct ttg
!
!      S   P   G   E   R   A   T   L   S   C   R   A   S   Q   G
7517  tct cca ggg gaa aga gcc acc ctc tcc tgc agg gcc agt cag Ggt
!
!      V   S   S   Y   L   A   W   Y   Q   Q   K   P   G   Q   A
7562  gtt agc agc tac tta gcc tgg tac cag cag aaa cct ggc cag gct
!
!      P   R   L   L   I   Y   D   A   S   S   R   A   T   G   I
7607  ccc agg ctc ctc atc tat gAt gca tcc aAc agg gcc act ggc atc
!
!      P   A   R   F   S   G   S   G   P   G   T   D   F   T   L
7652  cca gCc agg ttc agt ggc agt ggg Cct ggg aca gac ttc act ctc
!
!      T   I   S   S   L   E   P   E   D   F   A   V   Y   Y   C
7697  acc atc agc agC ctA gag cct gaa gat ttt gca gtT tat tac tgt
!
!      Q   Q   R   S   W   H   P   W   T   F   G   Q   G   T   R
7742  cag cag CGt aAc tgg cat ccg tgg ACG TTC GGC CAA GGG ACC AAG
!
!      V   E   I   K   R   T   V   A   A   P   S   V   F   I   F
7787  gtg gaa atc aaa cga act gtg gCT GCA Cca tct gtc ttc atc ttc
!
!      BsgI....
!
!      P   P   S   D   E   Q   L   K   S   G   T   A   S   V   V
7832  ccg cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg
!
!      C   L   L   N   N   F   Y   P   R   E   A   K   V   Q   W
7877  tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg

```

```

!
!      K   V   D   N   A   L   Q   S   G   N   S   Q   E   S   V
7922    aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc
!
!      T   E   R   D   S   K   D   S   T   Y   S   L   S   S   T
7967    aca gag cgg gac agc aag gac agc acc tac agc ctc agc agc acc
!
!      L   T   L   S   K   A   D   Y   E   K   H   K   V   Y   A
8012    ctg acG CTG AGC aaa gca gac tac gag aaa cac aaa gtc tac gcc
!      EspI.....
!
!      C   E   V   T   H   Q   G   L   S   S   P   V   T   K   S
8057    tgc gaa gtc acc cat cag ggc ctG AGC TCg ccc gtc aca aag agc
!      SacI....
!
!      F   N   R   G   E   C   .   .
8102    ttc aac agg gga gag tgt taa taa
!
!      GGCGCG CCaattctat ttcaaGGAGA cagtcata
8126
!      AscI..... RBS2.
!      (Amino acid sequence is SEQ ID NO: 588)
!      PelB signal sequence----- (22 codons) ----->
!      1   2   3   4   5   6   7   8   9  10  11  12  13  14  15
!      M   K   Y   L   L   P   T   A   A   A   G   L   L   L   L
8160    atg aaa tac cta ttg cct acg gca gcc gct gga ttg tta tta ctc
!
!      ...PelB signal-----> Start VH, FR1----->
!      16  17  18  19  20  21  22  23  24  25  26  27  28  29  30
!      A   A   Q   P   A   M   A   E   V   Q   L   L   E   S   G
8205    gcG GCC cag ccG GCC atg gcc gaa gtt CAA TTG tta gag tct ggt
!      SfiI..... MfeI...
!      NcoI....
!
!      31  32  33  34  35  36  37  38  39  40  41  42  43  44  45
!      G   G   L   V   Q   P   G   G   S   L   R   L   S   C   A
8250    ggc ggt ctt gtt cag cct ggt ggt tct tta cgt ctt tct tgc gct
!
!      ...FR1-----> CDR1-----> FR2----->
!      46  47  48  49  50  51  52  53  54  55  56  57  58  59  60
!      A   S   G   F   T   F   S   T   Y   E   M   R   W   V   R
8295    gct TCC GGA ttc act ttc tct act tac gag atg cgt tgg gtt cgC
!      BspEI..
!      BstXI...
!
!      FR2-----> CDR2 ----->
!      61  62  63  64  65  66  67  68  69  70  71  72  73  74  75
!      Q   A   P   G   K   G   L   E   W   V   S   Y   I   A   P
8340    CAa gct ccT GGt aaa ggt ttg gag tgg gtt tct tat atc gct cct
!      BstXI.....
!
!      ...CDR2-----> FR3----->
!      76  77  78  79  80  81  82  83  84  85  86  87  88  89  90
!      S   G   G   D   T   A   Y   A   D   S   V   K   G   R   F
8385    tct ggt ggc gat act gct tat gct gac tcc gtt aaa ggt cgc ttc
!
!      91  92  93  94  95  96  97  98  99 100 101 102 103 104 105
!      T   I   S   R   D   N   S   K   N   T   L   Y   L   Q   M
8430    act atc TCT AGA gac aac tct aag aat act ctc tac ttg cag atg

```



```

!
!           XbaI...
!           Supplied by extender-----
!
!           -----FR3----->
!           106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
!           N   S   L   R   A   E   D   T   A   V   Y   Y   C   A   R
! 8475      aac agC TTA AGg gct gag gac act gca gtc tac tat tgt gcg agg
!           AflII...
!           from extender----->
!
!           CDR3----->
FR4-->
!           121 122 123 124 125 126 127 128 129 130 131 132 133 134 135
!           R   L   D   G   Y   I   S   Y   Y   Y   G   M   D   V   W
! 8520      agg ctc gat ggc tat att tcc tac tac tac ggt atg GAC GTC tgg
!                                     AatII..
!
!           136 137 138 139 140 141 142 143 144 145
!           G   Q   G   T   T   V   T   V   S   S
! 8565      ggc caa ggg acc acG GTC ACC gtc tca agc
!                   BstEII...
!
!           CH1 of IgG1----->
!           A   S   T   K   G   P   S   V   F   P   L   A   P   S   S
! 8595      gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg gca ccc tcc tcc
!
!           K   S   T   S   G   G   T   A   A   L   G   C   L   V   K
! 8640      aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag
!
!           D   Y   F   P   E   P   V   T   V   S   W   N   S   G   A
! 8685      gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc
!
!           L   T   S   G   V   H   T   F   P   A   V   L   Q   S   S
! 8730      ctg acc agc ggc gtc cac acc ttc ccg gct gtc cta cag tCC TCA
!
! Bsu36I....
!
!           G   L   Y   S   L   S   S   V   V   T   V   P   S   S   S
! 8775      GGa ctc tac tcc ctc agc agc gta gtg acc gtg ccc tcc agc agc
! Bsu36I....
!
!           L   G   T   Q   T   Y   I   C   N   V   N   H   K   P   S
! 8820      ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc
!
!           N   T   K   V   D   K   K   V   E   P   K   S   C   A   A
! 8865      aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt GCG GCC
!
! NotI.....
!
!           A   H   H   H   H   H   H   G   A   A   E   Q   K   L   I
! 8910      GCa cat cat cat cac cat cac ggg gcc gca gaa caa aaa ctc atc
! ..NotI.... H6 tag..... Myc-Tag.....
!
!           S   E   E   D   L   N   G   A   A   q   A   S   S   A
! 8955      tca gaa gag gat ctg aat ggg gcc gca tag GCT AGC tct gct
!           Myc-Tag..... NheI...
!                               Amber
!

```

! III'stump

!

! Domain 3 of III

-----

!

! S G D F D Y E K M A N A N K G A  
8997 agt ggc gac ttc gac tac gag aaa atg gct aat gcc aac aaa GGC GCC  
! tcc t t t t t a g a c t t g g t

!W.T.

!

KasI...(2/4)

!

! M T E N A D E N A L Q S D A K G  
9045 atG ACT GAG AAC GCT GAC GAG aat gct ttg caa agc gat gcc aag ggt  
! c a t c t a c g c a g tct c t a c

!W.T.

!

! K L D S V A T D Y G A A I D G F  
9093 aag tta gac agc gTC GCG Acc gac tat GGC GCC gcc ATC GAc ggc ttt  
! a c t t tct t t t c t t t t t t c

!W.T.

!

NruI....

KasI...(3/4)

! I G D V S G L A N G N G A T G D  
9141 atc ggc gat gtc agt ggt tTG GCC Aac ggc aac gga gcc acc gga gac  
! t t c t tcc c c t t t t t t t t t t

!W.T.

!

MscI....(3/3)

! F A G S N S Q M A Q V G D G D N  
9189 ttc GCA GGT tcG AAT TCt cag atg gcC CAG GTT GGA GAT GGg gac aac  
! t t c t c a t a c t c t t t

!W.T.

!

BspMI.. (2/2)

XcmI.....

!

EcoRI...

! S P L M N N F R Q Y L P S L P Q  
9237 agt ccg ctt atg aac aac ttt aga cag tac ctt ccg tct ctt ccg cag  
! tca t t a t t c c t a t t a t c c t a

!W.T.

!

! S V E C R P F V F S A G K P Y E  
9285 agt gtc gag tgc cgt cca ttc gtt ttc tct gcc ggc aag cct tac gag  
! tcg t a t c t t c t agc t t a a t a

!W.T.

!

! F S I D C D K I N L F R  
9333 ttc aGC Atc gac TGC gat aag atc aat ctt ttC CGC  
! t tct t t t c a a c t a c t !W.T.

!

BstAPI.....

SacII...

!

End Domain 3

! G V F A F L L Y V A T F M Y V F  
9369 GGc gtt ttc gct ttc ttg cta tac gtc gct act ttc atg tac gtt ttc  
! t c t g t c t t a t t c c t t a t

!W.T.

!

start transmembrane segment

!

```

!       S   T   F   A   N   I   L       R   N   K   E   S
9417 aGC ACT TTC GCC AAT ATT TTA Cgc aac aaa gaa agc
!       tct  g   t   t   c   a c g       t   t   g   g tct !W.T.
!                                     Intracellular anchor.
!
!
!
9453          tag tga tct CCT AGG
!                               AvrII..
!
9468 aag ccc gcc taa tga gcg ggc ttt ttt ttt ct ggt
!       | Trp terminator |
!
! End Fab cassette
!
9503  ATGCAT CCTGAGG ccgat actgtcgtcg tcccctcaaa ctggcagatg
!       NsiI.. Bsu36I.(3/3)
9551 cacggttacg atgcgcccac ctacaccaac gtgacctatc ccattacggt
caatccgccg
9611 tttgttccca cggagaatcc gacgggttgt tactcgctca catttaatgt
tgaatgaaagc
9671 tggctacagg aaggccagac gcgaattatt tttgatggcg ttcctattgg
ttaaaaaatg
9731 agctgattta acaaaaattt aaTgcgaatt ttaacaaaat attaacgttt
acaATTTAAA
!
SwaI...
9791 Tatttgctta tacaatcttc ctgttttttg ggcttttctg attatcaacc GGGGTAcac
9850 ATG att gac atg cta gtt tta cga tta ccg ttc atc gat tct ctt gtt
tgc
!       Start gene II
9901 tcc aga ctc tca ggc aat gac ctg ata gcc ttt gtA GAT CTc tca aaa
ata
!
!                                     BglII...
9952 gct acc ctc tcc ggc atT aat tta tca gct aga acg gtt gaa tat cat
att
10003 gat ggt gat ttg act gtc tcc ggc ctt tct cac cct ttt gaa tct tta
cct
10054 aca cat tac tca ggc att gca ttt aaa ata tat gag ggt tct aaa aat
ttt
10105 tat cct tgc gtt gaa ata aag gct tct ccc gca aaa gta tta cag ggt
cat
10156 aat gtt ttt ggt aca acc gat tta gct tta tgc tct gag gct tta ttg
ctt
10207 aat ttt gct aat tct ttg cct tgc ctg tat gat tta ttg gat gtt !
! gene II continues
!----- End of Table -----

```

Please delete Table 37 and replace it with the following table:

! Table 37: DNA seq of w.t. M13 gene iii  
(Nucleotide sequenc is SEQ ID NO: 590; Amino acid sequence is SEQ ID NO: 591)

```

!
!       1   2   3   4   5   6   7   8   9  10  11  12  13  14  15
!       fM  K   K   L   L   F   A   I   P   L   V   V   P   F   Y
1579  gtg aaa aaa tta tta ttc gca att cct tta gtt gtt cct ttc tat

```

```

!       Signal sequence.....
!
!       16  17  18  19  20  21  22  23  24  25  26  27  28  29  30
!       S   H   S   A   E   T   V   E   S   C   L   A   K   P   H
! 1624 tct cac tcc gct gaa act gtt gaa agt tgt tta gca aaa ccc cat
! Signal sequence> Domain 1-----
!
!       31  32  33  34  35  36  37  38  39  40  41  42  43  44  45
!       T   E   N   S   F   T   N   V   W   K   D   D   K   T   L
! 1669 aca gaa aat tca ttt act aac gtc tgg aaa gac gac aaa act tta
! Domain 1-----
!
!       46  47  48  49  50  51  52  53  54  55  56  57  58  59  60
!       D   R   Y   A   N   Y   E   G   C   L   W   N   A   T   G
! 1714 gat cgt tac gct aac tat gag ggt tgt ctg tgG AAT GCt aca ggc
!                                     BsmI....
! Domain 1-----
!
!       61  62  63  64  65  66  67  68  69  70  71  72  73  74  75
!       V   V   V   C   T   G   D   E   T   Q   C   Y   G   T   W
! 1759 gtt gta gtt tgt act ggt gac gaa act cag tgt tac ggt aca tgg
! Domain 1-----
!
!       76  77  78  79  80  81  82  83  84  85  86  87  88  89  90
!       V   P   I   G   L   A   I   P   E   N   E   G   G   G   S
! 1804 gtt cct att ggg ctt gct atc cct gaa aat gag ggt ggt ggc tct
! Domain 1-----> Linker 1-----
!
!       91  92  93  94  95  96  97  98  99 100 101 102 103 104 105
!       E   G   G   G   S   E   G   G   G   S   E   G   G   G   T
! 1849 gag ggt ggc ggt tct gag ggt ggc ggt tct gag ggt ggc ggt act
! Linker 1----->
!
!       106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
!       K   P   P   E   Y   G   D   T   P   I   P   G   Y   T   Y
! 1894 aaa cct cct gag tac ggt gat aca cct att ccg ggc tat act tat
! Domain 2-----
!
!       121 122 123 124 125 126 127 128 129 130 131 132 133 134 135
!       I   N   P   L   D   G   T   Y   P   P   G   T   E   Q   N
! 1939 atc aac cct ctc gac ggc act taT CCG CCt ggt act gag caa aac
!                                     EciI....
! Domain 2-----
!
!       136 137 138 139 140 141 142 143 144 145 146 147 148 149 150
!       P   A   N   P   N   P   S   L   E   E   S   Q   P   L   N
! 1984 ccc gct aat cct aat cct tct ctt GAG GAG tct cag cct ctt aat
!                                     BseRI..
! Domain 2-----
!
!       151 152 153 154 155 156 157 158 159 160 161 162 163 164 165
!       T   F   M   F   Q   N   N   R   F   R   N   R   Q   G   A
! 2029 act ttc atg ttt cag aat aat agg ttc cga aat agg cag ggg gca
! Domain 2-----
!
!       166 167 168 169 170 171 172 173 174 175 176 177 178 179 180
!       L   T   V   Y   T   G   T   V   T   Q   G   T   D   P   V
! 2074 tta act gtt tat acg ggc act gtt act caa ggc act gac ccc gtt

```

```

!      Domain 2-----
!
!      181 182 183 184 185 186 187 188 189 190 191 192 193 194 195
!      K   T   Y   Y   Q   Y   T   P   V   S   S   K   A   M   Y
! 2119 aaa act tat tac cag tac act cct gta tca tca aaa gcc atg tat
!      Domain 2-----
!
!      196 197 198 199 200 201 202 203 204 205 206 207 208 209 210
!      D   A   Y   W   N   G   K   F   R   D   C   A   F   H   S
! 2164 gac gct tac tgg aac ggt aaa ttC AGa gaC TGc gct ttc cat tct
!                               AlwNI.....
!      Domain 2-----
!
!      211 212 213 214 215 216 217 218 219 220 221 222 223 224 225
!      G   F   N   E   D   P   F   V   C   E   Y   Q   G   Q   S
! 2209 ggc ttt aat gaG GAT CCa ttc gtt tgt gaa tat caa ggc caa tcg
!                               BamHI...
!      Domain 2-----
!
!      226 227 228 229 230 231 232 233 234 235 236 237 238 239 240
!      S   D   L   P   Q   P   P   V   N   A   G   G   G   S   G
! 2254 tct gac ctg cct caa cct cct gtc aat gct ggc ggc ggc tct ggt
!      Domain 2-----> Linker 2-----
!
!      241 242 243 244 245 246 247 248 249 250 251 252 253 254 255
!      G   G   S   G   G   G   S   E   G   G   G   S   E   G   G
! 2299 ggt ggt tct ggt ggc ggc tct gag ggt ggt ggc tct gag ggt ggc
!      Linker 2-----
!
!      256 257 258 259 260 261 262 263 264 265 266 267 268 269 270
!      G   S   E   G   G   G   S   E   G   G   G   S   G   G   G
! 2344 ggt tct gag ggt ggc ggc tct gag gga ggc ggt tcc ggt ggt ggc
!      Linker 2-----
!
!      271 272 273 274 275 276 277 278 279 280 281 282 283 284 285
!      S   G   S   G   D   F   D   Y   E   K   M   A   N   A   N
! 2389 tct ggt tcc ggt gat ttt gat tat gaa aag atg gca aac gct aat
! Linker 2>      Domain 3-----
!
!      286 287 288 289 290 291 292 293 294 295 296 297 298 299 300
!      K   G   A   M   T   E   N   A   D   E   N   A   L   Q   S
! 2434 aag ggg gct atg acc gaa aat gcc gat gaa aac gcg cta cag tct
!      Domain 3-----
!
!      301 302 303 304 305 306 307 308 309 310 311 312 313 314 315
!      D   A   K   G   K   L   D   S   V   A   T   D   Y   G   A
! 2479 gac gct aaa ggc aaa ctt gat tct gtc gct act gat tac ggt gct
!      Domain 3-----
!
!      316 317 318 319 320 321 322 323 324 325 326 327 328 329 330
!      A   I   D   G   F   I   G   D   V   S   G   L   A   N   G
! 2524 gct atc gat ggt ttc att ggt gac gtt tcc ggc ctt gct aat ggt
!      Domain 3-----
!
!      331 332 333 334 335 336 337 338 339 340 341 342 343 344 345
!      N   G   A   T   G   D   F   A   G   S   N   S   Q   M   A
! 2569 aat ggt gct act ggt gat ttt gct ggc tct aat tcc caa atg gct
!      Domain 3-----

```

```

!
!       346 347 348 349 350 351 352 353 354 355 356 357 358 359 360
!       Q   V   G   D   G   D   N   S   P   L   M   N   N   F   R
! 2614  caa gtc ggt gac ggt gat aat tca cct tta atg aat aat ttc cgt
!       Domain 3-----
!
!       361 362 363 364 365 366 367 368 369 370 371 372 373 374 375
!       Q   Y   L   P   S   L   P   Q   S   V   E   C   R   P   F
! 2659  caa tat tta cct tcc ctc cct caa tcg gtt gaa tgt cgc cct ttt
!       Domain 3-----
!
!       376 377 378 379 380 381 382 383 384 385 386 387 388 389 390
!       V   F   S   A   G   K   P   Y   E   F   S   I   D   C   D
! 2704  gtc ttt agc gct ggt aaa cca tat gaa ttt tct att gat tgt gac
!       Domain 3-----
!
!       391 392 393 394 395 396 397 398 399 400 401 402 403 404 405
!       K   I   N   L   F   R   G   V   F   A   F   L   L   Y   V
! 2749  aaa ata aac tta ttc cgt ggt gtc ttt gcg ttt ctt tta tat gtt
!       Domain 3-----> Transmembrane segment-----
!
!       406 407 408 409 410 411 412 413 414 415 416 417 418 419 420
!       A   T   F   M   Y   V   F   S   T   F   A   N   I   L   R
! 2794  gcc acc ttt atg tat gta ttt tct acg ttt gct aac ata ctg cgt
!       Transmembrane segment-----> ICA--
!
!       421 422 423 424 425
!       N   K   E   S   .
! 2839  aat aag gag tct taa ! 2853
!       ICA-----> ICA = intracellular anchor
!
!----- End of Table
!-----

```

Please delete Table 38 and replace it with the following table:

Table 38: Whole mature III anchor M13-III  
derived anchor with recoded DNA

```

!
!       1   2   3
!       A   A   A   (SEQ ID NO: 594)
! 1       GCG gcc gca   (SEQ ID NO: 593)
!       NotI.....
!
!       4   5   6   7   8   9   10  11  12  13  14  15  16  17
!       H   H   H   H   H   H   G   A   A   E   Q   K   L   I
! 10      cat cat cat cac cat cac ggg gcc gca gaa caa aaa ctc atc
!
!       18  19  20  21  22  23  24  25  26  27  28  29
!       S   E   E   D   L   N   G   A   A   .   A   S
! 52      tca gaa gag gat ctg aat ggg gcc gca Tag GCT AGC
!                               NheI...
!
!       30  31  32  33  34  35  36   37  38  39
!       D   I   N   D   D   R   M   A   S   T
! 88      GAT ATC aac gat gat cgt atg   gct tct act
! (ON_G37bot) [RC] 5'-c aac gat gat cgt atg gcG CAT Gct gcc gag aca g-3'
!       EcoRV..   (SEQ ID NO: 592)

```

```

! Enterokinase cleavage site.
!
! Start mature III (recoded) Domain 1 ---->
!      40 41 42 43
!      A E T V
! 118 |gcC|gaG|acA|gtC|
!      t a t t ! W.T.
!
!      44 45 46 47 48 49 50 51 52 53 54 55 56 57 58
!      E S C L A K P H T E N S F T N
! 130 |gaa|TCC|tgC|CTG|GCC|AaG|ccT|caC|acT|gaG|aat|AGT|ttC|aCA|Aat|
!      agt t t a a a c t a a tca t t c ! W.T.
!      MscI....
!
!      59 60 61 62 63 64 65 66 67 68 69 70 71 72 73
!      V W K D D K T L D R Y A N Y E
! 175 |gtg|TGG|aaG|gaT|gaT|aaG|acC|CtT|gAT|CGA|TaT|gC|aat|taC|gaA|
!      c a c c a t t a t c t c t g ! W.T.
!      BspDI...
!
!      74 75 76 77 78 79 80 81 82 83 84 85 86 87 88
!      G C L W N A T G V V V C T G D
! 220 |ggC|tgC|TtA|tgg|aat|gcC|ACC|GGC|GtC|gtT|gtC|TGC|ACG|ggC|gaT|
!      t t c g t a t a t t t t c ! W.T.
!      SgrAI..... BsgI....
!
!      89 90 91 92 93 94 95 96 97 98 99 100 101 102 103
!      E T Q C Y G T W V P I G L A I
! 265 |gaG|acA|caA|tgC|taT|ggC|ACG|TGg|gtG|ccG|atA|gGC|TTA|GCC|atA|
!      a t g t c t a t t t g c t t c ! W.T.
!      PmlI.... BlpI.....
!
! Domain 1-----> Linker 1----->
!      104 105 106 107 108 109 110 111 112 113 114 115 116 117 118
!      P E N E G G G S E G G G S E G
! 310 |ccG|gaG|aaC|gaA|ggC|ggC|ggT|AGC|gaA|ggC|ggT|ggC|AGC|gaA|ggC|
!      t a t g t t c tct g t c t tct g t ! W.T.
!
! Linker 1-----> Domain 2----->
!      119 120 121 122 123 124 125 126 127 128 129 130 131 132 133
!      G G S E G G G T K P P E Y G D
! 355 |ggT|GGA|TCC|gaA|ggA|ggT|ggA|acC|aaG|ccG|ccG|gaA|taT|ggC|gaC|
!      c t t g t c t t a t t g c t t ! W.T.
!      BamHI.. (2/2)
!
!      134 135 136 137 138 139 140 141 142 143 144 145 146 147 148
!      T P I P G Y T Y I N P L D G T
! 400 |acT|ccG|atA|CCT|GGT|taC|acC|taC|atT|aat|ccG|TtA|gaT|ggA|acC|
!      a t t g c t t t c c t c c c c t ! W.T.
!      SexAI....
!
!      149 150 151 152 153 154 155 156 157 158 159 160 161 162 163
!      Y P P G T E Q N P A N P N P S
! 445 |taC|ccT|ccG|ggC|acC|gaA|caG|aat|ccT|gcC|aaC|ccG|aaC|ccA|AGC|
!      T G t t t g a c c t t t t tct ! W.T.
!      HindIII...
!
!      164 165 166 167 168 169 170 171 172 173 174 175 176 177 178
!      L E E S Q P L N T F M F Q N N
! 490 |TTA|gaA|gaA|AGC|caA|ccG|TtA|aaC|acC|ttT|atg|ttC|caA|aaC|aaC|
!      c t G G tct g t c t t t c t g t t ! W.T.
! HindIII.
!
!      179 180 181 182 183 184 185 186 187 188 189 190 191 192 193
!      R F R N R Q G A L T V Y T G T
! 535 |CgT|ttT|AgG|aaC|CgT|caA|gGT|GCT|CtT|acC|gTG|TAC|Act|ggA|acC|

```

```

!      a g   c c a   t a g   g   g   a t a   t   t   t   g   c   t ! W.T.
!                                     HgiAI...      BsrGI...
!
!      194 195 196 197 198 199 200 201 202 203 204 205 206 207 208
!      V   T   Q   G   T   D   P   V   K   T   Y   Y   Q   Y   T
! 580 |gtC|acC|caG|GGT|ACC|gaT|ccT|gtC|aaG|acC|taC|taT|caA|taT|acC|
!      t   t   a   c   t   c   c   t   a   t   t   c   g   c   t ! W.T.
!                                     KpnI...
!
!      209 210 211 212 213 214 215 216 217 218 219 220 221 222 223
!      P   V   S   S   K   A   M   Y   D   A   Y   W   N   G   K
! 625 |ccG|gtC|TCG|AGt|aaG|gcT|atg|taC|gaT|gcC|taT|tgg|aat|ggC|aaG|
!      t   a   a   tca   a   c           t   c   t   c           c   t   a ! W.T.
!      BsaI....
!      XhoI....
!
!      224 225 226 227 228 229 230 231 232 233 234 235 236 237 238
!      F   R   D   C   A   F   H   S   G   F   N   E   D   P   F
! 670 |ttT|CgT|gaT|tgT|gcC|ttT|caC|AGC|ggT|ttC|aaC|gaa|gac|CCT|ttT|
!      C A a   C   c   t   c   t   tct   c   t   t   G   T   a   c ! W.T.
!
!      239 240 241 242 243 244 245 246 247 248 249 250 251 252 253
!      V   C   E   Y   Q   G   Q   S   S   D   L   P   Q   P   P
! 715 |gtC|tgC|gaG|taC|caG|ggT|caG|AGT|AGC|gaT|TtA|ccG|caG|ccA|CCG|
!      t   t   a   t   a   c   a   tct   tct   c   c   g   t   a   t   t ! W.T.
! 715 |DrdI.....|AgeI.....|
!
!      Domain 2-----> Linker 2----->
!      254 255 256 257 258 259 260 261 262 263 264 265 266 267 268
!      V   N   A   G   G   G   S   G   G   G   S   G   G   G   S
! 760 |GTT|AAC|gcG|ggT|ggT|ggT|AGC|ggC|ggA|ggC|AGC|ggC|ggT|ggT|AGC|
!      c   t   t   c   c   c   tct   t   t   t   tct   t   c   c   tct ! W.T.
! 760 |AgeI.....|
!      HpaI...
!      HincII.
!
!      Linker 2-----> Domain 3-->
!      269 270 271 272 273 274 275 276 277 278 279 280 281 282 283
!      E   G   G   G   S   E   G   G   G   S   G   G   G   S   G
! 805 |gaA|ggC|ggA|ggT|AGC|gaA|ggA|ggT|ggC|AGC|ggA|ggC|ggT|AGC|ggC|
!      g   t   t   c   tct   g   t   c   t   tct   g   t   c   tct   t ! W.T.
!
!      -----Domain 3----->
!      284 285 286 287 288 289 290 291 292 293 294 295 296 297 298
!      S   G   D   F   D   Y   E   K   M   A   N   A   N   K   G
! 850 |AGT|ggC|gac|ttc|gac|tac|gag|aaa|atg|gct|aat|gcc|aac|aaa|GGC|
!      tcc   t   t   t   t   t   a   g           a   c   t   t   g   g ! W.T.
!                                     KasI....
!
!      299 300 301 302 303 304 305 306 307 308 309 310 311 312 313
!      A   M   T   E   N   A   D   E   N   A   L   Q   S   D   A
! 895 |GCC|atg|act|gag|aac|gct|gac|gaG|AAT|GCA|ctg|caa|agt|gat|gCC|
!      t           c   a   t   c   t   a   c   g   a   g   tct   c   t ! W.T.
! 895 |KasI.....|BsmI.....|StyI...|
!
!      314 315 316 317 318 319 320 321 322 323 324 325 326 327 328
!      K   G   K   L   D   S   V   A   T   D   Y   G   A   A   I
! 940 |AAG|GGt|aag|tta|gac|agc|gTC|GCC|Aca|gac|tat|ggT|GCT|gcc|atc|
!      a   c   a   c   t   t   tct           t   t   t   c           t ! W.T.
! 940 |StyI.....|PflFI.....|
!
!      329 330 331 332 333 334 335 336 337 338 339 340 341 342 343
!      D   G   F   I   G   D   V   S   G   L   A   N   G   N   G
! 985 |gac|ggc|ttt|atc|ggc|gat|gtc|agt|ggt|ctg|gct|aac|ggc|aac|gga|
!      t   t   c   t   t   c   t   tcc   c   c   t           t   t   t   t ! W.T.

```



```

!      344 345 346 347 348 349 350 351 352 353
!      A   T   G   D   F   A   G   S   N   S
1030 | gcc|acc|gga|gac|ttc|GCA|GGT|tcG|AAT|TCt|
!      t   t   t   t   t   t   c   t           c ! W.T.
!                      BstBI...
!                      EcoRI...
!                      BspMI..
!
!      354 355 356 357 358 359 360 361 362 363
!      Q   M   A   Q   V   G   D   G   D   N
1060 | cag atg gcC CAG GTT GGA GAT GGg gac aac
!      a       t   a   c   t   c   t   t   t ! W.T.
!                      XcmI.....
!
!      364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379
!      S   P   L   M   N   N   F   R   Q   Y   L   P   S   L   P   Q
1090 | agt ccg ctt atg aac aac ttt aga cag tac ctt ccg tct ctt ccg cag
!      tca   t t a           t   t   c c t   a   t t a   t   c   c   t   a ! W.T.
!
!      380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395
!      S   V   E   C   R   P   F   V   F   S   A   G   K   P   Y   E
1138 | agt gtc gag tgc cgt cca ttc gtt ttc tct gcc ggc aag cct tac gag
!      tcg   t   a   t   c   t   t   c   t   t   agc   t   t   a   a   t   a ! W.T.
!
!      Domain 3----->
!      396 397 398 399 400 401 402 403 404 405 406 407
!      F   S   I   D   C   D   K   I   N   L   F   R
1186 | ttc aGC Atc gac TGC gat aag atc aat ctt ttC CGC
!      t tct   t   t   t   c   a   a   c t a           t
!                      BstAPI.....
!                      SacII...
!
!      transmembrane segment----->
!      408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423
!      G   V   F   A   F   L   L   Y   V   A   T   F   M   Y   V   F
1222 | GGc gtt ttc gct ttc ttg cta tac gtc gct act ttc atg tac gtt ttc
!      t   c   t   g   t   c t t a   t   t   c   c   t           t   a   t ! W.T.
!
!      424 425 426 427 428 429 430      431 432 433 434 435
!      S   T   F   A   N   I   L          R   N   K   E   S
1270 | aGC ACT TTC GCC AAT ATT TTA      Cgc aac aaa gaa agc
!      tct   g   t   t   c   a c g          t   t   g   g tct ! W.T.
!                      Intracellular anchor.
!
!      1306      tag tga tct CCT AGG
!                      AvrII..
!
!      1321 aag ccc gcc taa tga gcg ggc ttt ttt ttt ct ggt
!      | Trp terminator |
!
! End Fab cassette
! ----- End of Table -----

```

Please delete Table 39 and replace it with the following table:

Table 39: ONS to make deletions in III

! ONS for use with NheI

!

(SEQ ID NO: 595)

(ON\_G29bot)

! this is the reverse complement of 5'-c gTT gAT ATc gcT Agc cTA Tgc-3' ! 22

!

NheI... scab.....

```

(ON_G104top) 5'-g|ata|ggc|tta|gCT|aGC|ccg|gag|aac|gaa|gg-3' ! 30
(SEQ ID NO: 596)
! Scab.....NheI... 104 105 106 107 108
(ON_G236top) 5'-c|ttt|cac|agc|ggT|ttc|GCT|AGC|gac|cct|ttt|gtc|tgc-3' ! 37
(SEQ ID NO: 597)
! NheI... 236 237 238 239 240
(ON_G236tCS) 5'-c|ttt|cac|agc|ggT|ttc|GCT|AGC|gac|cct|ttt|gtc|Agc-
! NheI... 236 237 238 239 240
gag|tac|cag|ggT|c-3' (SEQ ID NO: 598)
! 50

! ONs for use with SphI G CAT Gc
(ON_X37bot) 5'-gAc TgT cTc ggc Agc ATg cgc cAT Acg ATc ATc gTT g-3' ! 37
(SEQ ID NO: 599)
! N D D R M A H A (SEQ ID NO: 601)
! (ON_X37bot)=[RC] 5'-c aac gat gat cgt atg gcG CAT Gct gcc gag aca gtc-3'
(SEQ ID NO: 600)
! SphI....Scab.....
(ON_X104top) 5'-g|gtG ccg|ata|ggc|ttG|CAT|GCa|ccg|gag|aac|gaa|gg-3' ! 36
(SEQ ID NO: 617)
! Scab.....SphI.... 104 105 106 107 108
(ON_X236top) 5'-c|ttt|cac|agc|ggT|ttG|CaT|gCa|gac|cct|ttt|gtc|tgc-3' ! 37
(SEQ ID NO: 602)
! SphI.... 236 237 238 239 240
(ON_X236tCS) 5'-c|ttt|cac|agc|ggT|ttG|CaT|gCa|gac|cct|ttt|gtc|Agc-
! NheI... 236 237 238 239 240
gag|tac|cag|ggT|c-3' (SEQ ID NO: 603)
! 50

```